

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 140623

TO: Janet Epps-Ford

Location: REM-2C05/2C18

Art Unit: 1635

Thursday, December 16, 2004 Case Serial Number: 08/901612 From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Epps-Ford,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527



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Schulwitz, Paul

From: Epps-Ford, Janet

Sent: Tuesday, December 14, 2004 2:36 PM

To: Schulwitz, Paul

Subject: Question regarding 08/901612...

Applicants in this case have amended the claims to add new sequence identifiers. The newly added sequences are variants of sequences already in the claims for example: original SEQ ID NO: 7 in the claim has the sequence agagatgattaggcagaggt

newly added SEQ ID NO: 58 in the claim has the sequence

agagatgauuaggcagaggt.

SEQ ID NO: 58 definitely has a similar structure as SEQ ID NO: 7, would the search for SEQ ID NO: 7 pick up hits that read on SEQ ID NO: 58?

Thanks.

Janet L. Epps-Ford, Ph.D.

Art Unit 1635

Mailbox: Remsen 2C18
Office: Remsen 2C05
Phone: 571-272-0757

Fax: 5

571-273-0757

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M76694 Hepatitis B
M76699 Hepatitis B
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Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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/mod_base=OTHER
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Magnetic glass particles, method for their preparation and uses
thereof
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Oligomucleorides specific for hepatitis B virus
Patent: US 5856459-A 7 05-JAN-1999;
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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Roche Diagnostics GmbH (DE)
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Sequence 7 from patent US 5856459.
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... Roberts, P.C., Goodchild, J., Craig, J. Charles. and
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Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
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Oligomucleotides specific for hepatitis B virus
Patent: US 5856459-A 8 05-JAN-1999;
Location/Qualifiers
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Patent: US 5856459-A 38 05-JAN-1999;
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/organism="unknown"
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Sequence 38 from patent US 5856459.
AR027810 30 bp
Sequence 8 from patent US 5856459.
AR027810 GI:5938630
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area virology 183 (2), 840-844 (1991)
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/product="precore protein"
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'note="Base substitution has
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/db_xref="taxon:10407"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="pre-C/C"
/note="Base substitution has occurred at this position in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
J (bases I to 93)
Galibert,F., and Charnay,P.,
Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
cloned in E. coli
Nature 281 (5733), 646-650 (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 93)
Li,J., Tong,S., Vitvitski,L., Zoulim,F. and Trepo,C.
Rapid detection and further characterization of infection with
hepatitis B virus variants containing a stop codon in the distal
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEPERICAA 93 bp DNA linear VRL 24-JAN
Hepatitis B virus variant B3 genomic RNA, entire pre-C region.
D30625 D01192
                                                                Stuyver, L., Schinazi, R., de Gendt, S., van Geyt, C., Zoulim, F., Fried, M. and Rossau, R.
A new genotype of hepatitis b virus
A new genotype of A 13-WAY-2001;
Patent: WO 0138 948 A 31-WAY-2001;
Pharmaset, Inc. (US); INNOGENETICS N.V. (BE)
Location/Qualifiers
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//coganism="Hepatitis B virus"
//mol_type="genomic DNA"
//db_xref="taxon:10407"
//note="HBeAg-negative HBV variant B3-pre-C region"
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                                                                                                                                                                                                                                                                                         6; Length 87;
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J. Gen. Virol. 71 (Pt 9), 1993-1998 (1990)
2212990
                                                                                                                                                                             1. .87
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                         ch 100.0%; Score 20; DB Similarity 100.0%; Pred. No. 16; 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="pre-C/C protein"
/protein_id="BAA06312.1"
/db_xref="G1:507810"
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                 synthetic construct
artificial sequences.
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synthetic construct
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Best Local Similarity
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KEYWORDS
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JOURNAL
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HPBPRECD 99 bp DNA linear VRL 11-MAY-1994 Hepatitis B virus type 4 precore protein (pre-C region, C) gene, 5'
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/note="g in wt; a in virus type 3 (creates internal stop
codon)"
                        e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                            Will,H.

Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
1853582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MQLFHLCLIISCSCPTFQASKLCLGWL"
                                                                                                                                                                                                                                                                   source text: Hepatitis B virus DNA.
                                                                                                                                                                                                                                                                                                                                                                                                         note="c in wt; t in virus type 3"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                      l. .99
/organism="Hepatitis B virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard_name="pre-C region"

    .99
    /organism="Hepatitis B virus"
/mol_type="genomic DNA"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon start=1
product="precore protein"
protein id="AAA45509.1"
db_xref="G1:485346"
                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10407"
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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          M76689.1 GI:485345
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/gene="C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="C"
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Best Local 8
      VERSION
KEYWORDS
SOURCE
ORGANISM
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                  /gene="C"
/note="g in wt; a in virus type 1 (creates internal stop
codon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="g in wt; a in virus type 2 (creates internal stop \operatorname{codon})"
                                                                                                                                                                                                                                                                                                                                                                                                                                e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                             Gaps
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area 91306476
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100.0%; Score 20; DB 14; Length 99;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hepatitis B virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Setandard name="pre-C region"
| Codon_start=1
| product="precore protein"
| protein id="AAA45581."
| db_xref="GI:485344"
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/gene="C"
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                                                                                                                                    Best Local Similarity
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                                                                                                                 Query Match
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HPBPRECB/c
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HPBPRECC/c
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JOURNAL MEDLINE

TITLE

PUBMED COMMENT FEATURES

REFERENCE AUTHORS gene

CDS

ORIGIN

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ACCESSION VERSION KEYWORDS

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Gaps

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HPBPRECF 99 bp DNA linear VRL 11-MAY-1994
Hepatitis B virus type 6 precore protein (pre-C region, C) gene, 5'
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Hepatitis B virus type 7 precore protein (pre-C region, C) gene, 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="C"
/note="t in wt; c in virus type 6 (loss of start codon)"
                                                                                                                                                                                                                                                                W76692.1 GI:485151
e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
91306476
                                                                                                                                                                                                                                                                                                                                                                                                     Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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 Length 99
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Hepatitis B virus DNA.
Location/Qualifiers
1. .99
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Query Match 100.0%; Score 20; DB 14; Best Local Similarity 100.0%; Pred. No. 16; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db_txref="taxon:10407"
/lo_.99
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/gene="C"
/product="precore protein"
/note="putative cds"
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                                                                                        1 AGAGATGATTAGGCAGAGGT 20
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Best Local Similarity 100.
Matches 20; Conservative
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/note="g in wt; a in virus type 5 (creates internal stop codon)"
95
                                                                                                                                                                                                                                  /note="g in wt; a in virus type 4 (creates internal stop codon)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e antigen, precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and Will,H.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                       /note="g in wt; a in virus type 4 (gly to asp)"
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                                                                                                                                                                                                                                                                                                                                         ; Score 20; DB 14; Length 99;
; Pred. No. 16;
0; Mismatches 0; Indels
                                                                                                                       /produčt="precore protein"
/protein_id="AAA4510.1"
/db_xref="GI.485348"
/trānslation="MQLFHLCLIISCSCPTVQASKLCLGWL"
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/db_xref="GI:485350"
/translation="MQLFHLCLIISCSCPTVQPSKLCLGWL"
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
10._.93
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                                                                                      'standard_name="pre-C region"
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/product="precore protein"
'db_xref="taxon:10407"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AGAGATGATTAGGCAGAGGT 23
                                                                                                          codon start=1
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100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                 /gene="C"
10. .93
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M76691.1 GI:485349
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/gene="C"
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HPBPRECI 99 bp DNA linear VRL 11-MAY-1994 Hepatitis B virus type 9 precore protein (pre-C region, C) gene, 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="c in wt; t in virus type 9 (creates internal stop codon)"
                                                                                                                                                                                                                                                                                                                                   e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10. .93
/gene="C"
/product="precore protein"
/standard_name="pre-C region note: putative CDS"
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                                         Query Match 100.0%; Score 20; DB 14; Length 99; Best Local Similarity 100.0%; Pred. No. 16; Matches 20; Conservative 0; Mismatches 0; Indels
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Hepatitis B virus
Hepatitis B virus
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/organism="Hepatitis B \
/mol_type="genomic DNA"
/db_xref="taxon:10407"
                                                                                                                    1 AGAGATGATTAGGCAGAGGT 20
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Hepatitis B virus type 11
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/gene="C"
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HPBPRECI/c
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HPBPRECK/c
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                                                                                                                                                                                                                                                                                                                                   /gene="C"
/note="g in wt; a in virus type 7 ( creates internal stop
codon)"
                                                                                                                                                                                                                                      /gene="C"
/note="a in wt; t in virus type 7 (loss of start codon)"
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e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
                                                                                                                                                                                  /product="precore protein"
/standard_name="pre-C region note: putative CDS"
                                                                                                                                                                                                                                                                              /gene="C" /note="a in wt; g in virus type 7 (gln to arg)" 92
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standard_name="pre-C region note: putative CDS"
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Pred. No. 16;
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   source text: Hepatitis B virus DNA.
Location/Qualifiers
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                                                     /organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db_xref="taxon:10407"
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/mol_type="genomic DNA"
/db_zref="taxon:10407"
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/gene="C"
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| Similarity 100.0%; Pr
20; Conservative 0;
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/gene="C"
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/gene="C"
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HPBPRECH/c
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/gene="C"
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/gene="C"
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                                                                                                                                                                                                                                                                                                                                                                             42. .43
/gene="C"
/note="frameshift mutation, deletion of single base in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                      Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. ar
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                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="precore protein"
/proteit="precore protein"
/proteit="GI:485533.1"
/translation="MQLFHLCLIISVHVILFKPPSCALGGFGTW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 20; DB 14; Length 99; Best Local Similarity 100.0%; Pred. No. 16; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                source text: Hepatitis B virus DNA. Location/Qualifiers
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                                                                                                                                                                   /organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db_xref="taxon:10407"
10._.99
/gene="C"
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
10. .99
/gene="C"
10. .>99
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus type 11"
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/gene="C"
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                                                                                                                                                                                                                                                                                    /gene="C"
/note="g in wt position 94; a in virus type 12 position
93"
                                                                                                                                                                                                                                     note="t in wt position 91; a in virus type 12 position
                                                                                                                                           'note="frameshift mutation, deletion of single base in
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e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area 91306476
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/product="precore protein"
/protein id="AAA45514.1"
/db_xref="G1:485560"
/translation="MQLPHLCLIISVHVLLFKPPSCALGGFRTW"
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Location/Qualifiers
1. .99
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/product="precore protein"
/protein_id="AAA45515.1"
/db_xref="G1:485362"
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Hepatitis B virus
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Matches 20; Conserv
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AF528206/c
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AF528207/c
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[Dages] to 150)

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Ganthe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Direct Submission

Submitted (11-1411-2012) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                           Schinazi, R., de Gendt, S., van Geyt, C., Zoulim, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/isolate="ASC1123"
/isolation source="ssymptomatic HBsAg carrier"
/specific_Tost="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. .>150
/note="contains partial basal core promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 20; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels
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Fried, M. and Rossau, R.
Fried, M. and Rossau, R.
A new genotype of hepatitis b virus
A new genotype of hepatitis b virus
D 0.03896. A. 3 11-MAY-2001;
Pharmasset, Inc. (US); INNOGENETICS N.V. (BE)
Location/Qualifiers
Location/Qualifiers
Location/Partic Construct*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="core antigen precursor"
/protein_id="AAP87556.1"
                                                                                                                                                                                                                                                                                                                                                 1. .129
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                         DNA
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                                                                                  Sequence 3 from Patent W00138498.
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                                                                                                                                       AX151114.1 GI:14533316
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AF528205.1 GI:32810971
                                                                                                                                                                      synthetic construct
synthetic construct
artificial sequences.
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                                                                 AX151114/c
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AF528205/c
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Hepatitis B virus ASC20 core antigen precursor, gene, partial cds.
AF528207
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Hepatitis B virus ASC1112 core antigen precursor, gene, partial
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                                                                                                                  Gaps
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/specific_nost="Homo sapiens"
/baref="taxon:10407"
/country="India"
/db_xref="G1:32810972"
/translation="MQLFHLCL11SCSCPTVQASKLCLGWLXG"
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/product="core antigen precursor"
/protein_id="maps7557.1"
/db_xref="GI:32810974"
/translation="MQLFHLCLISCSCPTVQASKLCLGWLXG"
                                                                            14; Length 150;
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/note="contains partial basal core promoter"
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100.0%; Pred. No. 15;
iive 0; Mismatches 0;
                                                                      ch 100.0%; Score 20; DB 1 Similarity 100.0%; Pred. No. 15; 20; Conservative 0; Mismatches
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/mol_type="genomic DNA"
/isolate="ASC1112"
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AF528206.1 GI:32810973
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/note="contains partial basal core promoter"
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/isolate="ASC58"
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Best Local Similarity
Matches 20; Conserv
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AF528209/c
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AF528210/c
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                                                                                          Unpublished

2 (Dases 1 to 150)

2 andhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Direct Submission

Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

(bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
Unpublished
                     1 (bases 1 to 150)
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus
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/specific_host="Homo saplens"
/db_xref="taxon:10407"
/country="India"
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/barcef="taxon:10407"
/country="India"
                                                                                                                                                                                                                                                                                                                                                                                                                       'note="contains partial basal core promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="core antigen precursor"
/protein id=AAR8758.1"
(db xref="GI:32810976"
/translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
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100.0%; Score 20; DB 14; Length 150;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels
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/note="contains complete precore region"
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/proviral
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/isolate="ASC340"
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/isolate="ASC20"
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Hepatitis B virus ASC58 core antigen precursor, gene, partial cds.
AF528209.1 GI:32810978
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Candhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
Unpublished
2 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
64. .>150
/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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AF528210.1 GI:32810980
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus
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/specific host="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
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/db_xref="GI:32810979"
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/note="contains complete precore region"
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/proviral
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100.0%; Pred. No. 15;
ive 0; Mismatches
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AF528212/c
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Hepatitis B virus ASC335 core antigen precursor, gene, partial cds.
AF528211
                                                                                                                                              2 (bases 1 to 150)
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
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       Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.

1 (bases 1 to 150)
Gandha, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (Dases I to 150)
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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                                                                                                                                                                                                                                                                                                                                                    /isolation_source="asymptomatic HBsAg carrier"/specific_host="Homo sapiens"
db_xref="taxon:10407"
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/specific_host="Homo sapiens"
/db_xref="taxon:10407"
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/note="contains partial basal core promoter"
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/note="contains complete precore region"
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/isolate="ASC335"
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Hepatitis B virus ASC343 core antigen precursor, gene, partial cds.
AF528312
AF528212.1 GI:32810983
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AF528213
AF528213.1 GI:32810985
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Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Direct Submission
Submitted (11-2002) Hepatitis Division, National Institute of Virology, 20-4, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe,S.S., Chadha,M.S., Wallmbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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/specific_Fost="Homo sapiens"
/barref="taxon:10407"
/country="India"
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                                                                                                                                                                               Length 150;
                                                                                               translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
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/note="contains partial basal core promoter"
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/db_xref="G1:32810982"
                                                                                                                                                                       Query Match
100.0%; Score 20; DB 14;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0;
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/isolate="ASC343"
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/codon_start=1
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Hepatitis B virus
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AF528215 150 bp DNA linear VRL 31-JUL-2003
Hepatitis B virus ASC424 core antigen precursor, gene, partial cds.
AF528215
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(bases 1 to 150)

Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Direct Submission

Submitted (11-JUL-2002) Hepatitis Division, National Institute of Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis B virus Hepathitis B virus Viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Red 1 (bases I to 150) Gandhe, S.S., (fladha, M.S., Walimbe, A.M. and Arankalle, V.A. Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
                                                                                                                                                                                                                                                                         Gaps
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/specific_host="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
  <1. .>150
/note="contains partial basal core promoter"
(64. .>150
/note="contains complete precore region"
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/note="contains partial basal core promoter"
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    organism="Hepatitis B virus"

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100.0%; Pred. No. 15;
ive 0; Mismatches
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Best Local Similarity 100.04
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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AF528216/c
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AF528215/c
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Hepatitis B virus ASC423 core antigen precursor, gene, partial cds.
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

(bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                             /isolation_source="asymptomatic HBsAg carrier"
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/country="India"
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/db_xref="taxon:10407"
/country="India"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains partial basal core promoter"
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/proviral
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AF528214.1 GI:32810987
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AF528218/c
LOCUS
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ACCESSION
VERSION
KEYWORDS
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Unpublished

2 (bases 1 to 150)

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Direct Submission

Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India

Location/Qualifiers
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2 (bases 1 to 150)
3 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUJ-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
                                                                                       Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
Hepatitis B virus ASC1035 core antigen precursor, gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus ASC1061 nonfunctional core antigen precursor,
gene, partial sequence.
AF528217
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/ppecific_host="Homo sapiens"/country="lndia"/country="lndia"
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/proviral
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                                                       GI:32810991
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Hepatitis B virus ASC339 core antigen precursor, gene, partial cds.
AF528218
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Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
                                                                                                                                          <1. .>150
/note="contains partial basal core promoter"
64. .>150
/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Gandhe, S. S. (hadha, W. S., Walimbe, A. W. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
/mol_type="genomic DNA"
/isolate="ASC1061"
/isolation source="asymptomatic HBsAg carrier"
/specific_host="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
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/specific_host="Homo sapiens"
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/country="India"
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/note="contains partial basal core promoter"
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/protein_id=AAR97566.1"
/db_xref="GI:32810995"
/trānslation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
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/isolate="ASC339"
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Best Local Similarity
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RESULT 34

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Hepatitis B virus ASC298 core antigen precursor, gene, partial cds. AF528222.1 GI:32810999
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/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/specific_host="Homo sapiens"
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     /isolation_source="asymptomatic HBsAg carrier"
/specific_host="Homo sapiens"
/barcef="taxon:10407"
/country="India"
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/note="contains partial basal core promoter"
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/note="contains partial basal core promoter"
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/isolate="ASC1029"
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AF528221/c
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Gandho, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (bases I to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus
Viruses, Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus ASC295 nonfunctional core antigen precursor, AF528219
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/db_xref="taxon:10407"
/country="India"
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/note="contains partial basal core promoter"
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/isolate="ASC295"
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/isolate="ASC1027"
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Best Local Similarity 100.
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Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae, Orthohepadnavirus.

E 1 (Dases 1 to 150)
S Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
E 2 (Dases 1 to 150)
S Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
L Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Anbeddar Road, Pune, Maharashtra 411001, India
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Submisted (11-UUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (Dases 1to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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/translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
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/note="contains complete precore region"
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/proviral
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                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/isolate="ASC298"
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AF528224/c
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Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
<1. .>150
//note="contains partial basal core promoter"
64. .>150
//note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases I to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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/country="India"
                                                                                                                                                                               100.0%; Score 20; DB 14; Length 150; 100.0%; Pred. No. 15; 0; Indels ive 0; Mismatches 0; Indels
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/note="contains partial basal core promoter"
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Similarity 100.0%; Pred. No. 15;
20; Conservative 0; Mismatches 0; Indels
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/proviral
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Best Local S:
Matches 20
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AF528228/c
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
                                                                                                                                    Chases I to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
                                               (bases 1 to 150)
Gandho,S.S., (Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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1 (bases 1 to 150)
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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                                 Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/isolation_source="asymptomatic HBsAg carrier"
/specific_host="Homo sapiens"
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/note="contains partial basal core promoter"
64. .>150
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/note="contains partial basal core promoter"
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AF528227.1 GI:32811005
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Hepatitis B virus ASC1072 nonfunctional core antigen precursor, gene, partial sequence.
AF528228.1 GI:32811006
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2 (bases 1 to 150)
2 adaha, M.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission (11-JUL-2002) Hepatitis Division, National Institute of Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus ASC1074 nonfunctional core antigen precursor, gene, partial sequence.
AF528229.1 GI:32811007
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/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus
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/specific_host="Homo sapiens"
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                                                                                            100.0%; Score 20; DB
100.0%; Pred. No. 15;
ive 0; Mismatches
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Matches 20; Conservative
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Similarity 100.0%; P: 20; Conservative 0;
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                          Unpublished
2 (bases 1 to 150)
2 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-15ub.2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
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Gandha, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Mandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional
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/specific_nost="Homo sapiens"
/ba xref="taxon:10407"
/country="India"
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/note="contains partial basal core promoter"
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/note="contains partial basal core promoter"
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Hepatitis B virus ASC265 nonfunctional core antigen precursor,
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2 (bases 1 to 150)

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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Gandho, S.S., (Anadha, W.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
                               Gaps
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Heparitis B virus ASC262 nonfunctional core antigen precursor, partial sequence.
AF528233.1 GI:32811011
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
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/specific_host="Homo sapiens"
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Pred. No. 15;
Mismatches
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                                                                                                                                                                                                                                                                                    gene, partial sequence. AF528232
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150 bp DNA linear VRL 31-JUL-2003
B virus ASC1275 core antigen precursor, gene, partial
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2 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Direct Submission
Submitted (11-UUJ-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus
Viruses; Fetroid viruses; Hepadnaviridae; Orthohepadnavirus.

(bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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2 (bases 1 to 150)
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /isolation_source="asymptomatic HBsAg carrier"
/specific_host="Homo sapiens"
/db_xref="taxon:10407"
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/note="contains partial basal core promoter"
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/note="contains complete precore region"
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        96 AGAGATGATTAGGCAGAGGT 77
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Hepatitis B virus ASC1109 nonfunctional core antigen precursor,
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Birect Submission, Direct Submitted (11-JUL-2002) Hepatitis Division, National Institute of Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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Gandho,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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VRL 31-JUL-2003

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SM Hepatitis B virus

Viruses, Retroid viruses; Hepadnaviridae, Orthohepadnavirus.

Viruses, Retroid viruses; Hepadnaviridae, Orthohepadnavirus.

E 1 (bases 1 to 150)

Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations

L Unpublished

E 2 (bases 1 to 150)

S Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.

Direct Submission

L Submitted (11-UUL-2002) Hepatitis Division, National Institute of virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Hepatitis B virus ASC1090 core antigen precursor, gene, partial
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
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core antigen precursor due to mutation"
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Matches 20; Conservative 0; Mismatches 0; Indels (

Search completed: December 15, 2004, 16:04:28 Job time : 764 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. ic search, using sw model cember 15, 2004, 09:10:16 ; Search time 181 Seconds (without alignments) 580.047 Million cell updates/sec	1tgattaggcagaggt 20 1tgattaggcagaggt 20 10.0, Gapext 1.0	Geneseq_23Sep04;* geneseqn1980s:* geneseqn1990s:* geneseqn2001as:* geneseqn2001as:* geneseqn2001as:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003bs:* i. geneseqn2003cs:* : geneseqn2004s:* : geneseqn2005cs:* : geneseqn2006s:* : geneseqn2006s	20 2 AAT72560 A8 20 2 AAT72561 A9 20 2 AAT72561 A9 30 2 AAT72561 A9 30 2 AAT72561 A9 30 2 AAT72563 A9 30 2 AAT72563 A9 40 40 40 40 40 40 40 40 40 40 40 40 40
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a "Internucleotide linkages are phosphorothioate"

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Hepatitis B virus RNA antisense oligonucleotide HBV43Ma

03-SEP-1997 (first entry)

AAT72561;

HBV; HBV infection; inhibition; replication; ss.

Location/Qualifiers

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Synthetic

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Roberts NA, Roberts PC, Slade A;
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 95.0
95.0
95.0
95.0
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misc_feature
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                                                                                                                                                                                                                                                                                                                           WO9639502-A1
                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                              12-DEC-1996
 119 119
                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                             AAT72560;
                                                                                                                   RESULT 1
0 0 0 0 0 0
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Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                                Mills JS;
                                                                                                                                                                                                                                                                Kilkuskie RE,
                                                                                                                                                                                                                                                                Jupp R,
                                                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE & CO AG F. (HYBR-) HYBRIDON INC.
                                                                                                                                                                                                                                                                ρ, Ą
                                                                                                                                                                                                                                                               Craig CJ, Frank BL, Goodchild
Roberts NA, Roberts PC, Slade
                                                                                                                                                                                                                                                                                              Claim 1; Page 12; 81pp; English.
                                                                                                                                                                                                                                            95US-00467397
                                                                                                                                                                                                                                                                           IPI; 1997-043124/04.
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Gaps

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AGAGATGATTAGGCAGAGGT 20

RESULT 2 AAT72561 AAT72561 ID AAT72561 standard; DNA; 20 BP.

1 AGAGATGATTAGGCAGAGGT 20

ð 셤 1 AGAGATGATTAGGCAGAGGT 20

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            The present sequence represents a synthetic oligonucleotide HBV43Ma which is complementary to a portion of the hepatitis B virus (HBV) RMA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non- contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single-stranded DNA probe comprising an anti-target nucleic acid, a (-)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising in 3'-5' order, an anti-target nucleic acid segment, a (-)-
promoter segment functionally linked to the anti-target segment, and a
nucleic acid reporter segment. The probe is useful for testing a sample
of a nucleic acid for the presence of a target nucleic acid segment or
for detecting a target nucleic acid segment in a sample. The probe may
also be used for the detection of hepatitis B virus (HBV). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which is used in an example from the present invention. (Updated on 15-
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter segment linked to the anti-target segment and a reporter segment, useful for detecting a target nucleic acid, e.g. hepatitis
                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes a single-stranded DNA probe (I)
                                                                                                                                                                              100.0%; Score 20; DB 2; Length 20; 85.0%; Pred. No. 5.8;
                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus; HBV; detection; probe; promoter; ss.
                                                                                                                                               Sequence 20 BP; 7 A; 1 C; 8 G; 1 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SP6 RNA polymerase promoter sequence SEQ ID NO:3.
                                                                                                                                                                                           85.0%; Pred. No. 5.8;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Col 19-20; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schumm JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                                                               1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-00652888
                                                                                                                                                                                                                                                                                                                                                                 AAA88131 standard; RNA; 25
                                                                                                                                                                   Query Match
Best Local Similarity 85.08
                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteria phage SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dimond RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-542420/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus, in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2003
13-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6100024-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hudson GR,
                                                                                                                                                                                                                                                                                                                                                                                                AAA88131;
                                                                                                                                                                                                                                                                                                                              RESULT 3
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The specification describes a composition of magnetic glass particles, which contain at least one magnetic object with a mean diameter between 5-500 nm. The composition is useful for the purification of nucleic acids. The composition can be used to process large quantities of nucleic acid samples, because it does not involve the particles being centrifuged or the fluids being drawn through glass fiber filters. PCR primers AAH25415-16 were used to amplify HBV DNA fragments. The amplified fragment can be
                                                                                                                                                                                                                                                                    /*tag= a
/note= "derivatisation with a p-(t-butyl)benzyl-residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of magnetic glass particles for purification of DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                     Magnetic glass particle; nucleic acid purification; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 20; DB 4; Length 27; Similarity 100.0%; Pred. No. 6; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                          Reverse PCR primer used to amplify a HBV DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27 BP; 5 A; 10 C; 2 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purified using the method of the invention
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 99; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geiger A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
        22
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AGAGAUGAUUAGGCAGAGGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGAGATGATTAGGCAGAGGT
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12-MAY-2000; 2000EP-00110165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA in automated processes.
                                                                            AAH25416 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT72562 standard; DNA; 30
                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weindel K, Riedling M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-381247/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                Hepatitis B virus.
                                                                                                                                                                                                                                                                                                           WO200137291-A1
                                                                                                                                                                                                                                           Key
modified_base
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                                                                                                                                22-AUG-2001
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                                                                                                      AAH25416;
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                                               RESULT 4
AAH25416/
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Hepatitis B virus RNA antisense oligonucleotide HBV88b.

Gaps

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// Score 20; DB 3; Length 25;
Pred. No. 5.9;
4; Mismatches 0; Indels

100.0%; 80.0%; P

Query Match 100. Best Local Similarity 80.0 Matches 16; Conservative

Sequence 25 BP; 10 A; 1 C; 10 G; 0 T; 4 U; 0 Other;

Mills JS;

Synthetic

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The present sequence represents a synthetic oligonucleotide HBV-87b which contains a sequence which is complementary to at least two non-contiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                     Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
"Internucleotide linkages are phosphorothioate"
                                                                                                                Kilkuskie RE,
                                                                                                                                                                                                                                                                                                                                                                                                                         th 100.0%; Score 20; DB 2; Length 30; Similarity 100.0%; Pred. No. 6; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus RNA antisense oligonucleotide HBV88Mb.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30 BP; 10 A; 2 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HBV, HBV infection; inhibition; replication; ss.
                                                                                                                Jupp R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "2'-0-methyladenosine"
                                                                 [Z4
                                                                                                         Frank BL, Goodchild J, Roberts PC, Slade A;
                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG (HYBR-) HYBRIDON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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note= "2'-OMe RNA"
                                                                                                                                                                                                                                   Claim 5; Page 15; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGAGATGATTAGGCAGAGGT 20
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                               95US-00467397.
   96WO-EP002432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT72563 standard; DNA; 30 BP
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/mod_base= gm
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mod_base= cm
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/note=
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                                                                                                                                                         WPI; 1997-043124/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
 04-JUN-1996;
                             06-JUN-1995;
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                                                                                                           Craig CJ, I
Roberts NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1997
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a synthetic oligonucleotide HBV88b which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                 /*tag= a
/note= "Internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                         Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "Internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                  Jupp R, Kilkuskie RE, Mills JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus RNA antisense oligonucleotide HBV-87b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 BP; 12 A; 3 C; 10 G; 5 T; 0 U; 0 Other;
HBV; HBV infection; inhibition; replication; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HBV; HBV infection; inhibition; replication; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                 (HOFF ) HOFFMANN LA ROCHE & CO AG F. (HYBR-) HYBRIDON INC.
                                                              Location/Qualifiers
1. .30
/*tag= a
                                                                                                                                                                                                                                                                                                                    Goodchild J,
PC, Slade A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AGAGATGATTAGGCAGAGGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 12; 81pp; English.
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Local Similarity 100.0%; Pr
les 20; Conservative 0;
                                                                                                                                                                                                         96WO-EP002432
                                                                                                                                                                                                                                      95US-00467397
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, Roberts PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-043124/04.
                                                             Key
misc_feature
                                                                                                                                        WO9639502-A1
                                                                                                                                                                                                     04-JUN-1996;
                                                                                                                                                                                                                                     06-JUN-1995;
                                                                                                                                                                                                                                                                                                                 Craig CJ, F
Roberts NA,
                                                                                                                                                                        12-DEC-1996
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Query Match

ò 엄 "mod_base= OTHER
'note= "2'-O-methyladenosine"

/*tag=

modified_base

*tag= £

WO9639502-A1 12-DEC-1996.

Synthetic

AAT72614;

RESULT 6 AAT72614

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Gaps

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The present sequence represents a synthetic oligonucleotide HBV88Mb which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
"Internucleotide linkages are phosphorothioate"
                                                                                                                                                                           Gaps
                                                                                                                                                                             ö
                                                                                                                                               Query Match
100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 85.0%; Pred. No. 6;
Matches 17; Conservative 3; Mismatches 0; IndelB
                                                                                                                                                                                                                                                                                                                                                                       Hepatitis'B virus RNA antisense oligonucleotide HBV-87Mb.
                                                                                                                           Sequence 30 BP; 12 A; 3 C; 10 G; 1 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                HBV; HBV infection; inhibition; replication; 88
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/mod_base= OTHER
/note= "2'-O-methyladenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
mod_base= OTHER
note= "2'-O-methyladenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/mod_base= OTHER
/note= "2'-0-methyladenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  '*tag= g
mod base= OTHER
note= "2'-O-methyladenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/*tag≂ b
/note= "2'-OMe RNA"
                                                                                                                                                                                                     1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                                                                                                                11 AGAGAUGAUUAGGCAGAGGT 30
 Claim 1; Page 12; 81pp; English.
                                                                                                                                                                                                                                                                                            ВР
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/mod_base= um
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/mod_base= um
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= d
/mod_base= gm
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/mod_base= gm
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                      AAT72615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mills JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kilkuskie RE,
                                                                                                                                                                                                                mod_base= OTHER
note= "2'-0-methyladenosine"
                                                                                     note = "2'-0-methyladenosine
                                                                                                                                                                                                                                                                                                                                                                        note= "2'-0-methyladenosine"
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                                                                                                                                                                                                                                                                                note= "2'-0-methyladenosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodchild J,
PC, Slade A;
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                                                                                                              *tag= j
mod_base= OTHER
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/mod_base= OTHER
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mod_base= OTHER
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mod_base= OTHER
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mod_base= OTHER
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/mod_base= um
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mod_base= gm
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mod_base= um
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/mod_base= um
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                         *tag=
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Roberts NA, Roberts
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Gaps

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The present invention describes a method of screening for an antiviral agent by the protein-priming activity of hepatitis B virus (HBV) DNA polymerase. Also described is developing an antiviral agent with a high selectivity to HBV which can be used for high-throughput screening. The present sequence represents an RNA oligonucleotide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single-stranded DNA probe comprising an anti-target nucleic acid, a (-)-promoter segment linked to the anti-target segment and a reporter segment, useful for detecting a target nucleic acid, e.g. hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a single-stranded DNA probe (I) comprising in 3'-5' order, an anti-target nucleic acid segment, a (-)-promoter segment functionally linked to the anti-target segment, and a nucleic acid reporter segment. The probe is useful for testing a sample of a nucleic acid for the presence of a target nucleic acid for probe also be used for the detection of hepatitis B virus (HBV). The probe also be used for the detection of hepatitis B virus (HBV). The present which is used in an example from the present invention. (Updated on 15-
                                  Screening of antiviral agents by protein-priming activity of hepatitis virus DNA polymerase.
                                                                                                                                                                                                                                                                                         DB 10; Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus; HBV; detection; probe; promoter; ds.
                                                                                                                                                                                                                                                   Sequence 39 BP; 5 A; 13 C; 3 G; 0 T; 18 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 64 BP; 14 A; 22 C; 4 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP6 RNA polymerase promoter sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 1
100.0%; Pred. No. 6.2;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Col 19-20; 18pp; English.
                                                                                    Disclosure; Page 12; 13pp; Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schumm JW;
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                                                                                                                                                                                                                                                                                                                                                              1 AGAGATGATTAGGCAGAGGT
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.v.
Thrhes 20; Conservative
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ID AAA88130 standard; DNA; 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteria phage SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fudson GR, Dimond RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-542420/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus, in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a synthetic oligonucleotide HBV-87Mb which contains a sequence which is complementary to at least two noncontigonus regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RNA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                                                  Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                                                 Mills JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       screening; antiviral; hepatitis B virus; HBV; DNA polymerase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus DNA polymerase related RNA oligonucleotide.
                                                                                                                                                                                                                                                                               Kilkuskie RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30 BP; 10 A; 2 C; 12 G; 3 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                 Jupp R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ryu WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB
85.0%; Pred. No. 6;
:ive 3; Mismatches
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PC, Slade A;
                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE & CO AG (HYBR-) HYBRIDON INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGAGAUGAUUAGGCAGAGGT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 15; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOGA-) MOGAM BIOTECHNOLOGY INST. (VIRO-) VIROGEN CO LTD.
                                          /mod base= um
                                                                                                                                                   96WO-EP002432.
                                                                                                                                                                                   95US-00467397.
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                        *tag= l
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                                                                                                                                                                                                                                                                                             Roberts PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                             Frank BL,
                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043124/04.
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Hepatitis B virus.
modified_base
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                                                                                                                                                 04-JUN-1996;
                                                                                                                                                                                  06-JUN-1995;
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Roberts NA,
                                                                          WO9639502-A1
                                                                                                           12-DEC-1996
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Matches

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ADC64742/

33 AGAGATGATTAGGCAGAGGT 14

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AAD09093 standard; DNA; 129

AAD09093/c

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The present invention relates to hepatitis B virus (HBV) strain FRI, genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreSI, preS2 and surface antigen HBBAG) and HBX proteins. HBV genotype G nucleic acids and surface artieful for diagnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to reat or prevent HBV genotype G infection. The HBV genotype G derived nucleic acids and antibodies are useful for detecting HBV genotype G in a sample or diagnosis of HBV genotype G infection. The presence of HBV genotype G infection. The presence of inver damage and/or liver cancer in the subject. The HBV genotype G core insert peptide encoding nucleic acid is useful for designing monitoring assays to study and predict the evolution of anti-HBe and anti-HBc antibodies and HBAG (genotype G e antigen) in patients infected with HBV. The antibodies or antigens of HBV genotype G are useful for identifying a stage of liver disease caused by HBV genotype G. The present sequence is a tagge of liver disease caused by HBV genotype G DNA fragment encoding e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zoulim F, Fried M;
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                    HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; HBeAg; liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.
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                                                                                                                                                                                                                                                                                                                             Hepatitis B virus FR1 strain genotype G HBeAg DNA fragment.
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100.0%; Score 20; DB 3; Length 64; 100.0%; Pred. No. 6.6; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stuyver L, Schinazi R, De Gendt S, Van Geyt C,
                                                                            1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 57; 84pp; English.
                                                                                                    23 AGAGATGATTAGGCAGAGGT 4
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                                                                                                                                                                                                             AAD09094 standard; DNA; 87
                                                                                                                                                                                                                                                                                         (first entry)
                                        20; Conservative
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              Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200138498-A2.
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                                                                                                                                                                                                                                                                                         04-SEP-2001
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  Query Match
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Zoulim F, Fried M;

Van Geyt C,

De Gendt S,

(PHAR-) PHARMASSET INC. (INNO-) INNOGENETICS NV. Stuyver L, Schinazi R,

21-NOV-2000; 2000WO-US032108. 24-NOV-1999; 99US-0167206P.

31-MAY-2001.

HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.

Hepatitis B virus. WO200138498-A2

Hepatitis B virus FR1 strain genotype G DNA fragment #1.

(first entry)

04-SEP-2001

AAD09093;

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The present invention relates to hepatitis B virus (HBV) strain FR1,
genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1,
PreS2 and surface antigen HBAAG) and HBX proteins. HBV genotype G nucleic
acids and polypeprides are useful for diagnosing, prognosing and treating
infections caused by HBV genotype G. They can be used in a vaccine to
infections caused by HBV genotype G infection. The HBV genotype G derived
nucleic acids and antibodies are useful for detecting HBV genotype G in a
sample or diagnosis of HBV genotype G infection. The presence of HBV
genotype G statistically correlates with the presence of liver damage
cond/or liver cancer in the subject. The HBV genotype G core insert
petide encoding nucleic acid is useful for designing monitoring assays
to study and predict the evolution of anti-HBe and anti-HBc antibodies
and HBAAG (genotype G e antigen) in patients infected with HBV. The
antibodies or antigens of HBV genotype G are useful for identifying a
stage of liver disease caused by HBV genotype G. The present sequence is
a tage of liver disease caused by HBV genotype G DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
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1es 20; Conservative
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Matches
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ABK29867 standard; DNA; 250 BP.

ABK29867/c ID ABK29 XX RESULT 13

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Gaps

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1 AGAGATGATTAGGCAGAGGT 20

20; Conservative

Best Local Similarity

Matches

Query Match

transgenic;

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cancer;
                                                                                                                                                                                                                                                      HBV promoter; vancomycin-resistant enterococci promoter; VRB promoter; vanH promoter; androgen receptor promoter; AR promoter; human epidermal growth factor receptor 2 promoter; her2 promoter;
                                                                                                                                                                                                                                                                                                                                                                                       Deta lactanase promoter; Bla promoter; transgene; cancer; breast cancolon cancer; immunological disorder; prostate cancer; cytostatic; autoimmune disease; HBV pre-8 promoter; Green expression modulator; multiple sclerosis; MS; chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma; systematic lupus erythematosus; SLB; graft-vs-host disease; GVHD; familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
                                                                                                                                                                                                 Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
                                                                                                Wild type hepatitis B virus core promoter.
(first entry)
23-APR-2002
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Hepatitis B virus.

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/*tag= c
/bound_moiety= "HNF3-2"
/note= "Hepatocyte nuclear factor 3-2"
                               /bound_moiety= "HNF4"
/note=""Hepatocyte nuclear factor 4"
Location/Qualifiers
                       æ
                       *tag=
        misc binding
                                                    misc_binding
                                                                                                   misc_binding
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WO200194600-A2

13-DEC-2001

06-JUN-2001; 2001WO-US018343

06-JUN-2000; 2000US-0209549P.

(GENE-) GENELABS TECHNOLOGIES INC.

Starr DB, Tam AW, Laurance MB, Michelotti BF; MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT; Bruice TW; Kim JP, s Velligan N Lim MY, E

WPI; 2002-130595/17.

New nucleic acid regulatory sequences, which are able to regulate expression of a gene operably linked to a promoter, useful for regulating the expression of transgenes and for treating e.g., cancer and immunological diseases.

22-JUN-2001; 2001WO-GB002817. 22-JUN-2000; 2000GB-00015308. 06-OCT-2000; 2000GB-00024544.

WO200198333-A2.

27-DEC-2001.

(CELL-) CELLTECH PHARM LTD.

Page M, Li J, Pumpens P;

WPI; 2002-098223/13.

P-PSDB; AAE17018.

Disclosure, Fig 1A; 95pp; English.

The invention describes an isolated nucleic acid regulatory sequence for a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci (VRE) promoter, an HBV promoter, andragon receptor (AR) promoter, Human epidermal growth factor receptor 2 (HBR2) promoter, or a beta lactamase (Bla) promoter. Transcription regulatory sequences may be used to regulate expression of the endogenous, autologous or heterologous genes operably linked to the promoter, and may be incorporated into heterologous nucleic acid constructs for use in regulated expression of transgenes. Regulated expression of cyclin D1 can be used in cancer therapies, such as breast, colon or pancreatic cancers and familial adenomatous polyposis. Regulation of the activity of CD40L gene promoter may be used in the treatment of immunological disorders, such as autoimmune diseases e.g. multiple solerosis (MS), systematic lupus erythematosus (SLE), graft, ve-host disease (GVHD) and rheumatoid

New proteins comprising a modified hepatitis B core antigen, useful as a vaccine in prophylactic or therapeutic vaccination of the human or animal body, particularly against hepatitis B virus infection.

Disclosure; Page 38-39; 40pp; English.

The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBCAg) wherein one or more of the four arginine repeats has been deleted and the protein comprising the C-terminal cysteine of HBCAg. The deleted region may be replaced by an epitope from a protein other than HBCAg, in which case the HBCAg acts as a carrier to

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arthritis. Regulated expression of genes under the control of the HBV (hepatitis B)-specific core, pre-S and X promoters can be used in the therapy of HBV disease, chronic hepatic insufficiancy, cirrhosis, hepatocellular carcinoma, and in the regulated expression of liver specific genes. Regulated expression of the vanH gene promoter can be used in treatment of Enterococcus infection, while regulated expression of the androgen receptor gene can be used in the treatment of prostate cancer. This sequence represents the hepatitis B virus core promoter the regulatory regions of which are described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus; HBV; core antigen; HBCAg; immune system; typhoid; prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes; hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea; tuberculosis; polio; rabies; acquired immunodeficiency syndrome; AIDS; dengue fever; yellow fever; malaria; whooping cough; salmonellosis; food poisoning; meningitis; gonorrhea; antiviral; antibacterial;
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus (HBV) core antigen (HBcAg) encoding DNA #1.
                                                                                                                                                                            100.0%; Score 20; DB 6; Length 250; 100.0%; Pred. No. 7.6; ive 0; Mismatches 0; Indels
                                                                                                                                                  Sequence 250 BP; 66 A; 59 C; 62 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                       229
                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .639
/*tag= a
/product= "HBcAg"
                                                                                                                                                                                                                                                                    248 AGAGATGATTAGGCAGAGGT
                                                                                                                                                                                                                                         1 AGAGATGATTAGGCAGAGGT
                                                                                                                                                                                                                                                                                                                             AAD27422/c
ID AAD27422 standard; DNA; 639
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                          20; Conservative
                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiprotozoal; ds
                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                          AAD27422;
                                                                                                                                                                              Query Match
                                                                                                                                                                                                            Matches
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          therapeutic acid is useful as a vaccine or in a method of prophylactic or therapeutic vaccination of the human or animal body, particularly against HBV. The nucleic acid encoding the protein may be used in gene therapy or DNA vaccination protocols. The chimeric protein or its nucleic acid may also be used as the basis of a prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth disease, polio, herpes, rabies, acquired immunodeficiency syndrome (AIDS), dengue fever, yellow fever malaria, tuberculosis, whooping cough, salmonallosis, typhoid, food poisoning, diarrhoea, meningitis or genorrhea. The present sequence is a DNA encoding Hepatitis B virus core antigen (HBCAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B (HB) core antigen fusion proteins, useful as vaccines for the prophylactic or therapeutic treatment of humans or animals against e.g. HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-and-
present the epitope to the immune system. This chimeric protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis; therapeutic; vaccine; acquired immune deficiency syndrome; influenza; polio; herpes; rabies; AIDS; foot-and-mouth disease; ds.
                                                                                                                                                                                                                                                                       Gape
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0
                                                                                                                                                                                                                                    100.0%; Score 20; DB 6; Length 639; 100.0%; Pred. No. 8.4; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                        Seguence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus core antigen (HBcAg) encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88. .636
/*tag= c
/product= "Mature HBc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stuart D, Rowlands D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .639
/*tag= a
/product= "HBc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 23-24; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                     1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                 33 AGAGATGATTAGGCAGAGGT 14
                                                                                                                                                                                                                                                                                                                                                                                                                   AAD31509 standard; DNA; 639 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2001; 2001WO-GB001607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2000; 2000EP-00107118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L. .87
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEDE-) MEDEVA EURO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gehin A, Gilbert R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-239995/29.
P-PSDB; AAE19793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200177158-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JJN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
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The present invention relates to hepatitis B virus (HBV) core antigen

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(HBCAg) fusion proteins and polynucleotides encoding such proteins. Sequences of the invention are useful in methods of prophylactic or therapeutic vaccination or to manufacture medicaments for prophylactic or therapeutic vaccination of the human or animal body against HBV, e.g. against viral hepatitis. They are also useful as a prophylactic vaccine against viral hepatitis. They are also useful as a prophylactic vaccine against e.g. hepatitis or virus, influenca, pollo, herpes, rables, acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The present sequence is a DNA encoding hepatitis B virus core antigen (HBCAg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Introducing nucleic acid molecules to an animal or human, useful for treating diseases including cancer, genetic diseases, arthritis or AIDS comprises administering a composition comprising two or more gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of introducing nucleic acid molecules to an animal which comprises administering a composition comprising two or more gene delivery vehicles to an animal at the same time and same site via a single administration device. The method is useful for introducing nucleic acid molecules to an animal, preferably humans for
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                            ö
                                                                                                                                                                          100.0%; Score 20; DB 6; Length 639; 100.0%; Pred. No. 8.4; ive 0; Mismatches '0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; precore/core; cancer; genetic disease; arthritis; AIDS.
                                                                                                                                            Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 23; 72pp; English.
                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                      33 AGAGATGATTAGGCAGAGGT 14
                                                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                                                                                                                                                        1 AGAGATGATTAGGCAGAGGT
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89US-00395932.
90US-00565606.
90US-00586603.
91US-00800328.
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920S-00965084.
930S-001021385.
93US-00104424.
93US-0012454.
93US-00125944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2001; 2001US-00821662
                                                                                                                                                                                                                                                                                                                                                       ADL56756 standard; DNA; 646
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    HBV precore/core DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JOLL/) JOLLY D J.
(MONT/) MONTISANO D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-282522/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               delivery vehicles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004063652-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-1988;
18-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1993
18-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                     ADL56756;
                                                                                                                                                                                                                                                                                                                      RESULT 16
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containing the entire precore/core region, into the BamHI site of KSII+. The precore/core region of plasmid KSII+HBpc/p was sequenced and was found to contain a single base pair deletion which causes a frameshift at codon 79 which results in two consecutive in-frame TAG codons. This deletion was corrected by PCR overlap extension in plasmid SK+ HBe using mutation may also be corrected using the primers given in AAQ47019-23 in a separate series of reactions. The isolated HBV precore/core region may therapeutic cytotoxic T-lymphocyte (TID) response, and a humoral response for the treatment of hepatitis B and C infections, as well as hepatocellular carcinomas. (Updated on 25-MAR-2003 to correct PN field.)

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Gaps .; 0

0; Indels

100.0%; Score 20; DB 2; Length 655; 100.0%; Pred. No. 8.5;

0; Mismatches

Best Local Similarity 100. Matches 20; Conservative

Query Match

1 AGAGATGATTAGGCAGAGGT 20

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Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

(Updated on 27-AUG-2003 to correct OS field.)

us-08-901-612a-7.rng

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treating diseases including cancer, genetic diseases, arthritis or AIDS.
The method can also be administered to plants using traditional methods.
The introduction of multiple or more than one nucleic acid molecule at one time provide significant advantages because multiple nucleic acid molecules can provide complementary substances or activities to a single corgan or joint. The difficulty, cost and time to engineer multiple corgan or joint. The difficulty, cost and time to engineer multiple nucleic acid molecules is much less than engineering a single molecule. With the use of multiple molecules, there is less chance that one substance or activity will sterically hinder or otherwise interfere with the use of multiple molecules or activities also permits the expression of different substances or activities from expression systems subject to differing activating events, thus permitting better control of differential expression of the different substances or activities. The present sequence represents the HBV precore/core DNA.
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Precore; core; coding region; hepatitis B; virus; HBV; plasmid; KSII+; KSII+HBpc/c; pAMG; deletion; frameshift; PCR; overlap extension; SK+ HBe; primers; mutation; hepatocellular carcinomas; class-I; cytotoxic T-lymphocyte; CTL; hepatitis C; infection; ss.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "Nucleotide which is deleted in plasmid pAM6"
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 12; Length 646; 100.0%; Pred. No. 8.5;
                                                                                                                                                                                                                                           Sequence 646 BP; 154 A; 170 C; 137 G; 185 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HBV (adw) corrected precore/core sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                                           AAQ47014 standard; DNA; 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
31-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9315207-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ47014;
                                                                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 17
    $$$$$$$$$$$$$$$$$$$$$$$
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Precore; core region; HBV; hepatitis B virus; gene delivery vehicle; GDV; mimunogen; HBV antigen; hepatitis C cardinoma cell; HBV infection; gene expression; non-tumourigenic tumour associated antigen; therapy; altered ras gene; altered psi gene; altered mucin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the precore/core region of the hepatitis B virus (HBV) genome. This sequence can be included in a gene delivery vehicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Introduction of nucleic acid molecules to an animal - comprises administration of two or more gene delivery vehicles comprising heterologous nucleic acid.
                                                                                                                                                                                                                  10. .97
/*tag= a
/note= "precore region"
98. .655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 131; 161pp; English.
                                                                                                                                                                                                                                                                           /note= "core region"
                                                                                                                                                                                                       Location/Qualifiers
                踞.
AAT35649/c
ID AAT35649 standard; cDNA; 655
                                                                                                                                                                                                                                                                                                                                                                         94US-00368210.
                                                                                                                                                                                                                                                                                                                                                  95WO-US016964
                                                                                               Precore/core region of HBV.
                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON VIAGENE INC.
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Jolly DJ, Montisano D;
                                                                                                                                                                                                                                                                 /*tag=
                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-333990/33.
                                                                                                                                                                               Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                              22-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1994;
                                                                                                                                                                                                                  misc feature
                                                                                                                                                                                                                                                   misc_feature
                                                          27-AUG-2003
25-FEB-1997
                                                                                                                                                                                                                                                                                                  WO9621015-A2
                                                                                                                                                                                                                                                                                                                         11-JUL-1996.
                                    AAT35649;
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Treatment of hepatitis B and C, and associated carcinoma(s) - using vector construct directing the expression of part of hepatitis B or

ņ Odea

Townsend K,

Lee WT,

Chang SMW,

Jolly DJ,

WPI; 1993-258682/32

(VIAG-) VIAGENE INC.

93WO-US001009. 92US-00830417

04-FEB-1993; 04-FEB-1992; This sequence represents the entire precore/core coding region of hepatitis B virus (HBV) isolated from the plasmid KSII+HBpc/c. This plasmid was created by ligating a 1.8 kb fragment of plasmid pAM6

Example 2; Fig 2; 110pp; English.

antigen.

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antigen. The GDVs can be used in the method of the invention, for introducing nucleic acids into an animal, by administration of a composition comprising two or more GDVs, in combination with a carrier or diluent. Each GDV contains a nucleic acid molecule not naturally contained within the GDV, or directs expression of at least one substance (or biologically active nucleic acid) in host cells containing the GDV. The two GDVs collectively direct the expression of at least two different substances, or direct the expression of at least one substance, where the GDVs differ in one or more biological functions. The GDVs can be used for destroying hepatitis C carcinoma cells, for treating HBV (when a GDV contains an immunogenic HBV fragment such as this sequence). The GDVs can be used for directing expression of non-tumourigenic, tumour associated antigens (such as altered ras gene), altered p53 gene, and altered mucin. (Updated on 27-AUG-2003 to correct OS field.)
(GDV) of the invention, and is used as an immunogenic portion of a HBV
88666666666666666888888
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Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

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100.0%; Score 20; DB 2; Length 655; 100.0%; Pred. No. 8.5; 0; Mismatches 0; Indels
                                                             1 AGAGATGATTAGGCAGAGGT 20
                                                                                         24
                                                                                 43 AGAGATGATTAGGCAGAGGT
                                20; Conservative
                  Local Similarity
      Query Match
                                 Matches,
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Gaps

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AAH77569 standard; DNA; 655 BP AAH77569; HBV genotype G strain US1 preCore/Core DNA.

19-OCT-2001 (first entry)

Hepatitis B virus, HBV; preCore; Core; preSl; preS2; HBS; HBX; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBeAg; ds.

Hepatitis B virus.

WO200140279-A2

07-JUN-2001.

20-NOV-2000; 2000WO-EP011526.

99EP-00870252 03-DEC-1999; 07-DEC-1999;

(INNO-) INNOGENETICS NV.

Stuyver L, Van Geyt C,

De Gendt S;

WPI; 2001-374785/39

Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy

Claim 3; Fig 7; 94pp; English.

The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in sequence with 32% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by

The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention relates to a fully defined sequence of 3248 mucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polymucleotides are useful for HBV genotyping. The proteins encoded by the polymucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting the proteins and should gain the proteins are useful for detecting the proteins and for detecting the proteins and surface against the proteins are useful for detecting the proteins and for detecting the proteins are also useful for preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRZ, USI, US3,

Claim 3; Fig 7; 94pp; English

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                           sample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting the Brotains and for detecting the Brotains and the detecting the preparing and HBeAg (precover precursor proteins). They are also useful for preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVKPS) and 7 strains (FRI, FR2, US1, US3, US3, US3, US3, US1, US3, US2, US1) of HBV genotype G
polynucleotides are useful for detecting antibodies in a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 4; Length 655; 100.0%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                        Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HBV genotype G strain FR2 preCore/Core DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Gendt S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 AGAGATGATTAGGCAGAGGT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР
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07-DEC-1999; 99US-0169287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH77568 standard; DNA; 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stuyver L, Van Geyt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INNO-) INNOGENETICS NV.
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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20

1 AGAGATGATTAGGCAGAGGT 33 AGAGATGATTAGGCAGAGGT

AAH77573 standard; DNA; 655

RESULT 22

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Gaps

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AAH77573,

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Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                 Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBV; HBPO1; HBSAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
                                  ch 100.0%; Score 20; DB 4; Length 655; Similarity 100.0%; Pred. No. 8.5; 20; Conservative 0; Mismatches 0; Indels
                 Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;
                                                                                                                                                                                  HBV genotype G strain US10 preCore/Core DNA
US6, US7, US9, US10) of HBV genotype G
                                                                                                                                                                                                                                                                                                                                                   De Gendt
                                                                             1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                              AAH77574 standard; DNA; 655 BP
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 7; 94pp; English.
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                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                  Stuyver L, Van Geyt C,
                                                                                                                                                                                                                                                                                                                                (INNO-) INNOGENETICS NV.
                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                    Hepatitis B virus.
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                                                                                                                                                AAH77574;
                                                                                                                                                                                                                                                                                                                                                                                                             therapy
                                                                                                                                                                                                                    HBeAg;
                                                                                                            RESULT 21
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the invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBW genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies directed against the proteins are useful for the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting the proteins and vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of preCore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRZ, USI, US3, US3, US3, US3, US3).
                                                                                                                                Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBK; HBPol; HBSAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg; HBeAg; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                  HBV genotype G strain US7 preCore/Core DNA.
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99US-0169287P.
                                                                (first entry)
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tes 20; Conserv
                                                                                                                                                                                                      Hepatitis B virus.
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07-DEC-1999;
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                                AAH77573;
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Matches
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RESULT 23

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Gaps

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Query Match 100.0%; Score 20; DB 4; Length 655; Best Local Similarity 100.0%; Pred. No. 8.5; Matches 20; Conservative 0; Mismatches 0; Indels

Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

HBV genotype G strain US5 preCore/Core DNA.

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Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBX; HBPol;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting the proteins and for detecting HBCAg and HBCAg (precore precursor proteins). They are also useful for preparing a vaccine or medicament for treating HBV infections. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                         Hepatitis B virus; HBV; preCore; Core; preSl; preSl; HBS; HBX; HBPol;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
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                                                                                                                                                                                            HBV genotype G strain US3 preCore/Core DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     De Gendt S;
                                 AAH77570 standard; DNA; 655 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2000; 2000WO-EP011526.
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                                                                                                                                          19-OCT-2001 (first entry)
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                                                                                    AAH77570;
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AAH77570/C
XX
AC
AAH7757
XX
AC
XX
ABBA91
XX
HBBA91
XX
HBA91
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Novel isolated and/or purified hepatitis B virus polypeptide and polymucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and

Claim 3; Fig 7; 94pp; English

therapy

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De Gendt

(INNO-) INNOGENETICS NV. Stuyver L, Van Geyt C, WPI; 2001-374785/39.

20-NOV-2000; 2000WO-EP011526. 03-DEC-1999; 99EP-00870252. 07-DEC-1999; 99US-0169287P.

07-JUN-2001

Hepatitis B virus. WO200140279-A2

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                                                                                                                                                                                            100.0%; Score 20; DB 4; Length 655; 100.0%; Pred. No. 8.5;
                                                                                                                                                                          Sequence 655 BP; 138 A; 154 C; 140 G; 195 T; 0 U; 28 Other;
                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus adw strain precore/core mutant DNA.
                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                      1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                                                                                                                                                AGAGATGATTAGGCAGAGGT 14
                                                                                                                                                                                                                                                                                                           AAD21244 standard; DNA; 655
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                              AAD21244;
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Matches
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AAD21244/c
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Gaps ö

> 1 AGAGATGATTAGGCAGAGGT 20 AGAGATGATTAGGCAGAGGT 14

33

20; Conservative

Matches

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Local Similarity

rhinovirus; pox virus; canary pox virus; vaccinia virus; influenza virus; adenovirus; adenovarius; adenovarius; adenovarius; adenovarius; parvovirus; adenovarius; nimunodeficiency virus; berpes virus; hepatotropic; ds; precore/ore DNA.

us-08-901-612a-7.rng

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The present invention relates to a method for treating hepatitis B or C directs the expression of at least one immunogenic portion of hepatitis B virus (HBV) antigen, containing HBeAg, HbcAg, HbsAg, S, Pre-S1, Pre-S2, open reading frame (ORF) 5, ORF 6, HBV pol or HBxAg or co-expression of a HBV antigen and at least one immunogenic portion of a HBV antigen and at least one immunogenic portion of a hepatitis C virus (HCV) antigen. The vectors are useful in gene therapy, particularly for treating or preventing hepatitis F and hepatitis C infections, as well as hepatoccellular carcinomas (HCC). The present sequence is a PCR primer used for amplifying Hepatitis B virus adw strain precore/core mutant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New vectors that direct the (co-)expression of one or more immunogenic portions of the hepatitis B or C virus antigen(s), useful in gene therapy, e.g. for treating or preventing hepatitis B or C infections, or hepatocellular carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DB 4; Length 655; 100.0%; Pred. No. 8.5;
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replace(338. .340, CAA)
/*tag= d
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/*tag= a
/note= "Precore region'
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/note= "Core region"
replace(332. .334, CC)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  92US-00830417.
93US-00032385.
93US-00102132.
94US-00286829.
95US-00374414.
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Best Local Similarity 100...
Then 20; Conservative
                                                                                        98. .655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-647290/74.
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                 misc_feature
                                                                                        misc_feature
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                                                                                                                                                          mutation
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ABX80077/C
ID ABX800
XX
AC ABX800
XX
XX
XX
XX
XX
HEPATIT
XW
HEPATIT
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Treating hepatitis C infections in a warm-blooded animal by administering a vector construct, which directs the expression of an immunogenic portion of a hepatitis C antigen, and alternatively, with an

immunomodulatory cofactor.

O'dea J;

Townsend K,

Lee WTL,

Chang SMW,

Jolly DJ,

(ODEA/) LEEW/)

WPI; 2003-174125/17.

JOLLY D J.
CHANG S M W.
LEE W T L.
TOWNSEND K.
O'DEA J.

(JOLL/) (CHAN/)

92US-00830417. 93US-00032385. 93US-00102132. 94US-00286829. 95US-00374414.

17-MAR-1993; 04-AUG-1993;

05-AUG-1994;

04-FEB-1992;

07-JUN-1995;

24-JUL-2001; 2001US-00912679.

Hepatitis B virus.

US2002141974-A1.

03-OCT-2002

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The invention relates to a method for treating hepatitis C infections in directs the expression of at least one immunogenic portion of a hepatitis C antigen, where an immune response is generated, and alternatively, in combination with an immunomodulatory cofactor. The invention also relates in a vector construct which directs the co-expression of at least one immunogenic portion of a hepatitis B antigen and at least one immunogenic portion of a hepatitis B antigen and the postion of the polyprotein antigen, an immunogenic portion of the polyprotein antigen, an immunogenic portion of the polyprotein antigen and an immunosegulatory cofactor. A recombinant virus carrying the vector construct is selected from poliovirus, rhinovirus, pox virus, canary pox virus, vaccinia virus, adenovirus, adenovirus, andenovirus, carrying the vector virus, vaccinia virus, adenovirus, and and an immunogenia with a virus, adenovirus, carrying the vector virus, vaccinia virus, adenovirus, and virus, adenovirus, and virus, and virus, adenovirus, and virus, and vir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGAGATGATTAGGCAGAGGT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 2; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX96938 standard; DNA; 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
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ID ABX96938
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AC ABX9693
XC ABX9695
XT I5-MAY
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Hepatitis B virus, hepatitis C virus, hepatitis C infection, poliovirus, hepatitis B infection, hepatitis C antigen; polyprotein antigen; SV40;

Hepatitis B virus precore/core DNA.

22-APR-2003 (first entry)

ABX80077;

δ 셤 *tag= c note= "This is labelled 'preCore'"

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. .658

*tag= d note= "This labelled 'Core'"

*tag= a product= "Precore antigen"

. 659 4. .82

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cocation/Qualifiers
                                                                                   /*tag= 6
2. .100
/*tag= 0
Hepatitis B virus.
                                                                                                          misc_feature
                                                                                                                                                                                                                                       misc_feature
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12-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO8901518-A.
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                                                                                                                                                                                                                                                                                                                                                                        conflict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for treating intracellular infections within warm-blooded animals comprising administering to a warm-blooded animals comprising administering to a warm-blooded animal a vector construct which directs the expression of at least one immunogenic portion of an intracellular pathogen, and a protein having the immunogenic portion of the antigen to generate an immunor response. The method is useful for treating intracellular infections or diseases including viral infections (e.g. hepatitis B virus (HBV), hepatitis C virus (HCV), herpes simplex virus (HSV), human immunodeficiency virus (HIV) or feline immunodeficiency virus (FIV)), parasitic infections (e.g. rickettsia, leishmaniasis or malaria) and certain bacterial diseases (e.g. legionella, tuberculosis or chlamydia). This sequence represents hepatitis B virus DNA used in the method of the
               Human; HBV; HCV; gene; ds; hepatitis B virus; hepatitis C virus; intracellular infection; HSV; HIV; viral infection; herpes simplex virus; human immunodeficiency virus; FIV; feline immunodeficiency virus; parasitic infection; rickettaia; malaria; leishmaniasis; tuberculosis; bacterial disease; legionella; chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating intracellular infections, e.g. viral, parasitic and bacterial diseases, comprises administering a vector construct which directs the expression of an immunogenic portion of an antigen from an intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence of subclones encompassing the core (C) and precore (preC) antigens (Ag) of an adw serotype hepatitis B (HB) virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus; core gene; precore gene; antigen; vaccine; polypeptide expression sequence; AcNPV transfer vector pAcYM1; pAcYM1KTpc; pAcYM1KTc; recombinant baculovirus; YM1KYpc; MX1KTc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 10; Length 655; 100.0%; Pred. No. 8.5; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 44-45; 69pp; English.
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ACCOUNTY
ACCOUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee WTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGAGATGATTAGGCAGAGGT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0%; P. Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                    99US-00466035.
                                                                                                                                                                                                                                                                                                                             97US-00931031
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sallberg M, Milich DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-288144/28.
                                                                                                                                                                                                                                                                                                                                                                      (SALL/) SALLBERG M. (MILI/) MILICH D R.
                                                                                                                                                                                                                                                                                                                                                                                            (MILI/) MILICH D R (LEEW/) LEE W T L.
                                                                                                                                                 Hepatitis B virus
                                                                                                                                                                                              US2002165172-A1.
                                                                                                                                                                                                                                                                                                                             16-SEP-1997;
                                                                                                                                                                                                                                                                                  17-DEC-1999;
                                                                                                                                                                                                                                         07-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen.
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The coding sequences of the preC and C Ags of HB virus were inserted into Autograph californica nuclear polyhedrosis virus (AcNPV) transfer vector Autograph californica nuclear polyhedrosis virus (AcNPV) transfer vector and ACVANIXTO and PACYMIXTO and pACYMIXTO and pACYMIXTO cannot the Callowing cotransfection with infectious ACNPV DNA, recombinant baculoviruses were obtained - YMIXYC and YMIXYC. It was determined that all the HBCAG and HBpCAG was cell associated and that the yield of purified HBCAG was of the order of 5 mg per liter of 1x10(9) infected cells. Such Ag may be useful in vaccines. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contg. two
                                                                                                                '*tag= f f note= "Differs from the HB virus adw sequence published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New plasmid replicon for inserting several genes into vector - copolypeptide expression structures, and derived viral vectors for infecting insect cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 1; Length 660; Pred. No. 8.5;
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                                                                                                                                                                      by Ono and associates (1983)"
181. .182
                           *tag= b
product= "Core Antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page ?; 74pp; English.
                                                                                                                                                                                                                                                                                                                    /*tag= h
/note= "As above"
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/note= "As above"
                                                                                                                                                                                                                                         *tag= g
note= "As above"
                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "As above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "As above"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87GB-00019108
88GB-00016084
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01. .658
                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1989-068873/09.
P-PSDB; AAP90702.
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Best Local Similarity
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Page 16

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Gaps

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0; Indels

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Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                       Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
  0; Mismatches
                                                                                                                                     HBV genotype G strain US6 preCore/Core DNA.
                                                                                                                                                                                                                                                                                                                De Gendt S;
                   1 AGAGATGATTAGGCAGAGGT 20
                                    46 AGAGATGATTAGGCAGAGGT 27
                                                                         AAH77572/c
ID AAH77572 standard; DNA; 664 BP
                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 7; 94pp; English.
                                                                                                                                                                                                                                              20-NOV-2000; 2000WO-EP011526.
                                                                                                                                                                                                                                                                  99EP-00870252
99US-0169287P
                                                                                                                     (first entry)
20; Conservative
                                                                                                                                                                                                                                                                                                              Van Geyt C,
                                                                                                                                                                                                                                                                                           (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                               WPI; 2001-374785/39.
                                                                                                                                                                                           Hepatitis B virus.
                                                                                                                                                                                                             WO200140279-A2,
                                                                                                                                                                                                                                                                 03-DEC-1999;
07-DEC-1999;
                                                                                                                     19-0CT-2001
                                                                                                                                                                                                                              07-JUN-2001
                                                                                                                                                                                                                                                                                                               Stuyver L,
                                                                                                   AAH77572;
Matches
                                                               RESULT 29
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The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention is pacification, a sequence of 3248 nucleotides as given in sequence. The patient is degenerate to the mentioned sequence. These polynucleotides are useful for HBV genotyping. The proteins encoded by sample. Ligands that bind to the proteins and antibodies directed against the polynucleotides are useful for detecting antibodies directed against the proteins are useful for detecting antibodies directed against the proteins are useful for detecting the proteins and subshape of the proteins and antibodies directed against the proteins are useful for detecting the proteins are useful for medicament for treating HBV infections. The preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRZ, USI, US3, US7, US9, USIO) of HBV genotype G
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Sequence 664 BP; 146 A; 160 C; 144 G; 208 T; 0 U; 6 Other;
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Gaps
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0
100.0%; Score 20; DB 4; Length 664; 100.0%; Pred. No. 8.5; o; Mismatches 0; Indels
              Local Similarity 100.
 Query Match
                 Best Loca
Matches
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1 AGAGATGATTAGGCAGAGGT 20
                         14
                 33 AGAGATGATTAGGCAGAGGT
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The present sequence is the DNA sequence of the hepatitis B virus core antigen (HBcAg) gene from HBV serotype ayw. A peptide comprising a HBV protein can be used in claimed methods of the invention for modulating an immune response in a mammal. A method of inducing a systemic immune response to a peptide in a mammal comprises transmucosally administering for the hammal a macromolecular aggregate of the peptide. The macromolecular aggregate comprises at least 10 peptide subunits, may have a molecular weight of over 1,000 kba, and is preferably at least 5 nm in diameter. It is resistant to digestive degradation, being stabilised in aggregate form by chemical treatment and/or by recombinant protein caggregate form hy chemical treatment and/or by recombinant protein or engineering of the peptide. The peptide preferably comprises a HBV comprises and HBV surface protein, nucleocapsid protein or engineering of the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response in the mammal. A method of suppressing an immune response in the mammal and which may be stabilised by that is resistant to digestive degradation and which may be stabilised by contal tolerance when induction of systemic immunity is undesirable, e.g. in cases of chronic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating a systemic immune response to a peptide in a mammal comprises transmucosally administering a macromolecular aggregate of the peptide.
                                                                                                                                                                                      HBcAg; immunomodulator; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                               /note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 1; 81pp; English.
                                                                                                                                                                                                                                                               Location/Qualifiers
10. .669
                                                                                                                                                    Hepatitis B virus core antigen DNA
                                                                                                                                                                                                                                                                                                                             "HBcAg"
                      7220/c
ADO07220 standard; DNA; 669 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2003; 2003WO-US033178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2002; 2002US-0419279P.
                                                                                                                                                                                                                                                                                                         /*tag= a
/product= '
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                               'partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-348329/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORAG-) ORAGEN CORP
                                                                                                                                                                                                                             Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                    WO2004035007-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AD007221
                                                                                                                15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michaels F;
                                                                        ADO07220;
RESULT 30
                    ADD07220/
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Gaps ö Sequence 669 BP; 155 A; 170 C; 148 G; 196 T; 0 U; 0 Other; 100.0%; Score 20; DB 12; Length 6 100.0%; Pred. No. 8.5; cive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 20, Conservative

.. 0

ò 셤 stage of liver disease caused by HBV genotype G. The present sequence is hepatitis B virus (HBV) strain FR1, genotype G DNA fragment encoding PreCore/Core antigen (HBCAg) protein

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Gaps

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0; Indels

0; Mismatches

20; Conservative

1 AGAGATGATTAGGCAGAGGT 20

100.0%; Score 20; DB 4; Length 673; 100.0%; Pred. No. 8.5;

Sequence 673 BP; 148 A; 165 C; 146 G; 214 T; 0 U; 0 Other;

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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                               Query Match
883333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl except= (pos:4. .6, aa:Xaa)
/transl_except= (pos:82. .84, aa:Xaa)
/note= "Xaa corresponds to in-frame stop codon; Does not
include stop codon"
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                                                                                                                                                                                                                                                                                                                            HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease; hepatitis; liver cancer; HBCAg; core antigen; ds.
                                                                                                                                                                                                                                                                       Hepatitis B virus FR1 strain genotype G PreCore/HBcAg DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         core protein"
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/note= "Core insert peptide DNA"
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/*tag= c
/note= "HBcAg core protein DNA"
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'note= "PreCore protein DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "PreCore/HBcAg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                       AAD09092 standard; DNA; 673 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-2000; 2000WO-US032108
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                                                                                                                                                                                                           04-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PHAR-) PHARMASSET INC. (INNO-) INNOGENETICS NV
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P-PSDB; AAE04707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                                                           Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBV); HBPOl; HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBcAg; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 675 BP; 149 A; 165 C; 147 G; 214 T; 0 U; 0 Other;
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33 AGAGATGATTAGGCAGAGGT 14
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                                                                                                          AAH77563 standard; DNA; 675
                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                         HBV preCore/Core gene
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                      Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                            WO200140279-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-DEC-1999;
07-DEC-1999;
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                                                                                                                                                AAH77563;
                                                                   RESULT 32
AAH77563/c
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AAH77567/c

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Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBPOl; HBAAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
                                                                                                                                                                                                                                                                                                                                                                                                                                 HBV genotype A strain HBVXCPS preCore/Core DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Gendt S;
      20
                                             33 AGAGATGATTAGGCAGAGGT 14
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                                                                                                                                                                                                                                  AAH77566 standard; DNA; 681 BP
      1 AGAGATGATTAGGCAGAGGT
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07-DEC-1999; 99US-0169287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                AAH77566;
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100.0%; Score 20; DB 4; Length 681; 100.0%; Pred. No. 8.5; ive 0; Mismatches 0; Indels Sequence 681 BP; 151 A; 166 C; 139 G; 189 T; 0 U; 36 Other; 100.0%; Local Similarity 100. 1es 20; Conservative Query Match Best Loc Matches

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AGAGATGATTAGGCAGAGGT 33

RESULT 34

(revised)
(first entry)

25-MAR-2003 19-NOV-1990

AAN80943;

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Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
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                                                HBV genotype G strain FR1 preCore/Core DNA.
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AAH77567 standard; DNA; 681 BP
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                                                                                                                                                                                                                                                                                 Claim 3; Fig 7; 94pp; English.
                                                                                                                                                20-NOV-2000; 2000WO-EP011526.
                                                                                                                                                                 99EP-00870252.
99US-0169287P.
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AAN80943 standard; DNA; 750
                                (first entry)
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                                                                                                                                                                                                          Van Geyt C,
                                                                                                                                                                                         (INNO-) INNOGENETICS NV
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                                                                                                 Hepatitis B virus.
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es 20; Conserv
                                                                                                                WO200140279-A2.
                                                                                                                                                                03-DEC-1999;
07-DEC-1999;
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                AAH77567;
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ID AAN8
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AC AAN8
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DT 25-M
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(ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
(NAIM-) NAT INST IMMUNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
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                                            WPI; 2002-009266/01
                          Singh M,
                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                          Kumar V,
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                                                                                                                                                                                                                                                                                       The cloned HBV DNA can be used to engineer plasmids for HBcAg synthesis in bacteria. The DNA may be fused to a gene for beta galactosidase. The recombinant protein can be used for immuno- assays, to raise antibodies, and in vaccines. See also AAN82265 and 66. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic mouse; cancer; oncogene; bicistronic hepatitis B virus; HBV;
XIS-c-myc transgene; hepatocellular carcinoma; malignant liver tumour;
XIS; c-myc; murine; HBX; carcinogen; ds.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                               Polynucleotide encoding HBEAG and HBCAG immuno-reactive polypeptide useful in immunoassays, for raising antibodies and as vaccine prods.
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                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 1; Length 750; 100.0%; Pred. No. 8.6; tive 0; Mismatches 0; Indels
                          Hepatitis B core antigen; virus; vaccine; immunoassay; ss.
                                                                                                                                                                                                                                                                                                                                                 Sequence 750 BP; 176 A; 192 C; 160 G; 222 T; 0 U; 0 Other;
                                                                                                                                                                                                    Staller JM;
                                                                                                                                                                                                   Mimms LT,
                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                          Disclosure; Page ?; 32pp; English.
                                                                                        /product= "HBcAg"
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         HBV core gene of plasmid pHBV-8.
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                                                                                                                                              87EP-00117370
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Best Local Similarity 100.(
Matches 20; Conservative
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                                                                                                                                                                                 (ABBO ) ABBOTT LAB
                                           Hepatitis B virus
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                                                                                                                                             25-NOV-1987;
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This polynucleotide represents the sequence of the regulatory and coding regions of the X15 component in the X-myc construct. The invention crastees to a bicistronic hepatitis B virus (HBW) X15-c-myc transgene, comprising of the HBV X15 gene and c-myc gene. The myc gene is known to be an activatable oncogene. The transgene encodes a truncated HBV X15 crotein, that has amino acids 58-154 of HBV X15 and a murine c-myc protein, respectively. A transgenic mouse containing the transgene construct is useful for screening a candidate substance (CS), to construct is useful for screening a candidate substance (CS), to construct by exposing a transgenic containing the transgene containing the mouse determined by exposing a transgenic couse to CS, and monitoring the mouse conformation to hepatocellular carcinoma in the transgenic mouse or to CS compared to the development of hepatocellular carcinoma in a conformation of the conformation of hepatocellular carcinoma in the conformation of hepatocellular carcinoma in the conformation of the carcinoma in the ca
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                                                                                                                                                                                                                                                         New bicistronic hepatitis B virus (HBV) X15-c-myc transgene, useful for producing transgenic mouse model systems for human hepatocellular carcinoma, comprises HBV X15 transgene and c-myc transgene.
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AAV82691 standard; DNA; 1334 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 3; 12pp; English.
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The present sequence represents part of the genome of a fulminant
Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.
The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the cambrace a mutation from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative required region, the enhancer II force upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the peptide amino acid change to Cys or Met. The HBV variants of the proteins and HBV nucleic acid. Probes that hybridise to any of the proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to detect HBV-related disease.
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                                                                  New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
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20; Conservative 0
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                            WPI; 1999-009329/01.
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Gaps

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0; Indels

100.0%; Score 20; DB 2; Length 1334;

0; Mismatches

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nucleic acid that has
             a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to P) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II (core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cyg or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, sepecially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
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0
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                                                                                                                                                                                                                                                                                                Sequence 1395 BP; 277 A; 387 C; 331 G; 398 T; 0 U; 2 Other;
  specification describes Hepatitis B virus (HBV)
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Best Local Similarity 100.
Matches 20; Conservative
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AAV82687/c
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B virus; variant; FHBV; HBV; binding interaction;

98WO-EP002048.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

WPI; 1999-009329/01.

Carman B;

The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.

Disclosure; Fig 5; 85pp; English.

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; ss.

Hepatitis B virus. WO9845421-A2. 98WO-EP002048. 97GB-00007221.

08-APR-1998; 09-APR-1997;

15-0CT-1998

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Carman B;

Fulminant hepatitis B virus genotype D variant FHBV2 sequence.

846 AGAGATGATTAGGCAGAGGT 827

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AAV82685 standard; DNA; 1445

AAV82685/

AAV82685;

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mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
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                                                                                       Score 20; DB 2; Length 1400;
Pred. No. 9.2;
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                                                   Sequence 1400 BP; 287 A; 388 C; 332 G; 393 T; 0 U; 0 Other;
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                                                                                                                                                                  1 AGAGATGATTAGGCAGAGGT 20
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                                                                                                                                                                                                                                                                                            AAV82692 standard; DNA; 1445 BP.
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Local Similarity 100.0%;
nes 20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reduce the ability to bind inhibitory proteins in the host cell
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AAV82690/c
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Matches
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16-FEB-1999 (first entry)

AAV82690;

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Gaps

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100.0%; Score 20; DB 2; Length 1445; 100.0%; Pred. No. 9.2; ive 0; Mismatches 0; Indels (

1 AGAGATGATTAGGCAGAGGT 20

20; Conservative

Matches

Query Match Best Local Similarity

Carman B;

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The present sequence represents part of the genome of a fulminant

The present sequence represents part of the genome of a fulminant

The specification describes Hepatitis B virus (HBV) nucleic acid that has

a mutation (i.e. alteration from the normal nucleotide in any of the

genotypes A to F) in at least two of the enhancer I region, the negative

regulatory element region, the enhancer II region, the negative

credulatory alement region, the enhancer II region, the negative

credulatory alement region, the enhancer of the

peptide amino acid change to (ys or Met. The HBV variants of the

proteins and HBV nucleic acid. Probes that hybridise to any of the

proteins and HBV nucleic acid. Probes that hybridise to any of the

specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to detect HBV-related disease.

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Specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to 
                                                                                                                                                                                                                                                                                                    New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fulminant hepatitis B virus genotype D variant CHBV2 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 2; Length 1445; 100.0%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1445 BP; 298 A; 400 C; 336 G; 411 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 5; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   846 AGAGATGATTAGGCAGAGGT 827
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                                                                              97GB-00007221.
                     98WO-EP002048.
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AAV82695 standard; DNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97GB-00007221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
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                                                                                                                                 (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                   WPI; 1999-009329/01.
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                  08-APR-1998;
                                                                           09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-1999
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                                                                                                                                                                                             Carman B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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               ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
                                                      Fulminant hepatítis B virus; variant; FHBV; HBV; binding interaction;
HBV-related disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Fulminant hepatitis B virus genotype D variant FHBV7 sequence.
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1 Similarity 100.0%; Score 20; DB 2; Length 1445;
20; Conservative 0; Mismatches من تسكمات
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 5; 85pp; English.
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                                                                                                                                                                                                                                                                                                                         98WO-EP002048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-009329/01.
                                                                                                                                             Hepatitis B virus.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      08-APR-1998;
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Gaps

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New hepatitis B virus nucleic acid with combination of specific mutations

WPI; 1999-009329/01.

Carman B;

WO9845421-A2 15-OCT-1998

AAV82684;

RESULT 43

Matches

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especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
                                                                                                                               The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negaliatory element region, the enhancer II core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the processing and regions are used to detect HBV-related disease.
- useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1500 BP; 308 A; 412 C; 347 G; 433 T; 0 U; 0 Other;
                                                                                     Disclosure; Fig 5; 85pp; English
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Gaps ö 100.0%; Score 20; DB 2; Length 1500; 100.0%; Pred. No. 9.3; 0; Indels Mismatches 846 AGAGATGATTAGGCAGAGGT 827 1 AGAGATGATTAGGCAGAGGT 20 ö g ઠે

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AAV82683 standard; DNA; 1500 16-FEB-1999 (first entry) HBV-related disease; ss. AAV82683; RESULT 45

Fulminant hepatitis B virus genotype D variant AHBV1 sequence.

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;

Hepatitis B virus.

WO9845421-A2

15-OCT-1998

98WO-EP002048. 08-APR-1998; 97GB-00007221. 09-APR-1997;

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure, Fig 5; 85pp; English.

The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to P) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory

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sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, septecially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                                                                                                                                                                                                                                                                      Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                               Fulminant hepatitis B virus genotype D variant HBVP2CSX sequence.
                                                                                                                                                                           ..
0
                                                                                                                                                  100.0%; Score 20; DB 2; Length 1500; 100.0%; Pred. No. 9.3;
                                                                                                                         Sequence 1500 BP; 305 A; 411 C; 354 G; 430 T; 0 U; 0 Other;
                                                                                                                                                                          0; Indels
                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                  846 AGAGATGATTAGGCAGAGGT 827
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                                                                                                                                                               Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   HBV-related disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus.
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The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the regulatory element region, the enhancer I region, the negative sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect they-related disease, especially fullminant infection, but also severe chronic infection or serologically fullminant forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell Sequence 1500 BP; 305 A; 408 C; 349 G; 438 T; 0 U; 0 Other;

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

(UNIU) UNIV GLASGOW

WPI; 1999-009329/01.

Carman B;

Disclosure, Fig 5; 85pp; English.

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;

HBV-related disease; ss

Hepatitis B virus. WO9845421-A2

Wild type hepatitis B virus genotype D nucleotides 1000-2500.

16-FEB-1999

AAV82706;

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Gaps

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AAV82706 standard; DNA; 1500 BP.

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The present sequence represents part of the genome of a fulminant the present sequence represents part of the genome of a fulminant. The specification describes Hepatitis B virus (HBV) mucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the spenitypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer I region, the negative sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the proteins and HBV nucleic acid. Probes that hybridise to any of the proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or servologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they also severe chronic infection or mutations are associated with fulminant infections, probably because they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
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                                                                                                                                                                                                                                                                                                                          Fulminant hepatitis B virus genotype D variant FHBV3 sequence.
       DB 2; Length 1500;
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                                           0; Indels
   100.0%; Score 20; DB
100.0%; Pred. No. 9.3
:ive 0; Mismatches
                                                                                                             846 AGAGATGATTAGGCAGAGGT 827
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                                                                             1 AGAGATGATTAGGCAGAGGT 20
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                                                                                                                                                                                                                                                                                        (first entry)
Query Match
Best Local Similarity 100.'
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      HBV-related disease; ss
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New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

97GB-00007221.

09-APR-1997;

15-0CT-1998.

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01.

Disclosure; Fig 5; 85pp; English.

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The present sequence represents part of the genome of wild type Hepatitis B virus genotype D, nucleotides 1000 to 2500. Mutations occur in this region in fullminant hepatitis B virus (FRBV) patients. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in a least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstram regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to change to Cys or Met. The HBV variants of the specified mutated regions are used to detect HBV-related disease, especially fulminant incleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1500 BP; 304 A; 409 C; 351 G; 436 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Best Local Similarity 100.
Matches 20; Conservative
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1D AAV8268
AC AAV8268
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DE 16.FEB.
XX
KY
KW Fulmin.
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Gaps

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Score 20; DB 2; Length 1500; Pred. No. 9.3;); Mismatches 0; Indels (

RESULT 48

1 AGAGATGATTAGGCAGAGGT 20

20; Conservative

Best Local Similarity

Matches

Query Match

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The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) mucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, to a mutation which leads to any sequence, basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or especially unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                         New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1500 BP; 314 A; 403 C; 343 G; 440 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          Disclosure; Fig 5; 85pp; English.
                    (UNIU ) UNIV GLASGOW
                                                                                                            WPI; 1999-009329/01.
                                                                Carman B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus (FRBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to P) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the Invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                                                                                                                                                                                                                                                                           New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents part of the genome of a fulminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 2; Length 1500; 100.0%; Pred. No. 9.3; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1500 BP; 302 A; 416 C; 353 G; 427 T; 0 U; 2 Other;
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                                                                                                                                                                                                                     97GB-00007221.
                                                                                                                                                                            98WO-EP002048
HBV-related disease;
                                                                                                                                                                                                                                                            (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                                                                                                               WPI; 1999-009329/01.
                                           Hepatitis B virus.
                                                                                                                                                                          08-APR-1998;
                                                                                                                                                                                                                     09-APR-1997;
                                                                                     WO9845421-A2
                                                                                                                                15-OCT-1998
                                                                                                                                                                                                                                                                                                             Carman B;
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                                  0; Indels
100.0%; Scc.
100.0%; Pred. No.
                                                                                                                 Search completed: December 15, 2004, 15:38:57 Job time : 185 secs
                                                                       1 AGAGATGATTAGGCAGAGGT 20
           Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Gaps

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846 AGAGATGATTAGGCAGAGGT 827

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AAV82693 standard; DNA; 1500 BP.

16-FEB-1999 (first entry)

AAV82693;

1 AGAGATGATTAGGCAGAGGT 20

Local Similarity 100.

Best Loca Matches

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; ss.

Hepatitis B virus.

AAV82693/ 1D AAV82693/ XX AAV8: XX I 16-F1 XX FULm: XX FULm: XX HEPU-: XX HEPU-:

WO9845421-A2

15-0CT-1998

98WO-EP002048.

08-APR-1998; 09-APR-1997;

97GB-00007221

Fulminant hepatitis B virus genotype D variant HBVP3CSX sequence.

Score 20; DB 2; Length 1500; Pred. No. 9.3;

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BZ350602 htts8d07.g AJ713073 AJ713073 AA503497 nh59g10.8 AJ572696 AJ572696 BX975154 Reverse 8 BE558110 f119f03.Y AZ336360 1M0066A09 AQ317545 RECIII-79 CB719936 AMGNNUC:N BE605742 f119f03.X	BQ122423 BST607999 CK76599 eca01-43m AQ491131 RPCI-11-2 AQ554673 RPCI-11-3 BJ650447 BD650447 CL186343 104 401 BO6642 CSRL-17167- CD304890 StrPu691. BH975438 OGH59802. BH973998 OGH59802. BH973998 OGH50C03. CK791475 4126207 B AZ519049 RPCI-11-7 BQ78214 UL-R-FF0- CL189821 104 407-1 BZ345634 h867c01.b CK100681 FOXWART 8 BZ058469 11633412.	B247 BX59 BX69 BQ99 BQ94 CC20 CC20 CC20 CC20 CC20 CC20 CC20 CC2	A2775622 ZM0008D05 A193589 ttf7904.x CE06404 ttg7-g88-CE064177 HD05E12w CE487389 tig7-g88-CE559021 CE4400_467 B0434994 60250759 CE92348 tig7-g88-A27804 tig7-g88-A280489 Mus muscu CE781116 tig7-g88-B1104 CT-MSP-206 A2473761 IM0289M18 B1833319 603087914 CF788155 B56899 MAAG359054 CC21555 CH264-383 CC221555 CH261-99K CC2166082 CM261-99K CC166082 CM261-99K AG359054 Mus muscu CC586584 CH240_383 CC221555 CH261-99K CC186082 CM261-99K AG359054 Mus muscu CC586584 CH240_383 CC221555 CH261-99K AG359054 Mus muscu CC586584 CH240_383 CC221555 CH261-99K AG359054 Mus muscu CC586584 CH261-99K AG359054 Mus muscu CC586584 CH240_383 CC221555 CH261-193 CC221555 CH261-193 AQ50321 CH261-11-3
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: December 15, 2004, 09:10:16; Search time 1339.5 Seconds 544.080 Million cell updates/sec	1-612A-7 3attaggcagaggt 20 NUC 0 , Gapext 1.0 seqs, 18219865908 residues isfying chosen parameters: 65645750 Match 0% Match 100%	EST:* 1: 9b est1:* 2: 9b est2:* 3: 9b_htc:* 4: 9b_est2:* 5: 9b_est5:* 7: 9b_est5:* 7: 9b_est5:* 8: 9b_gss1:* 9: 9b_gss2:* 9: 9b_gss2:* 8: 9b_gss2:* 9: 9b_gss2:* 8: 9b_gss2:* 9ceater than or equal to the score of the result being printed, derived by analysis of the total score distribution. SUMMARIES Ouery The Match Length DB ID Description	

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

LOCUS

RESULT 1 BG487106

98 c 100

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Use the control of c
                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:5379775"
/tissue type="tadpole"
/dev_stage="embryo, stages 40-45"
/lab_host="DHJD8 (phage-resistant)"
/clone_lib="NICHD XGC Emb8"
/note="vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV;
/note="vectorionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
                                           Xenopus tropicalis (western clawed frog)
Sanopus tropicalis
Sanopus tropicalis
Sanopus tropicalis
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
I (bases 1 to 587)
NIH-XCG http://image.llnl.gov/image/html/xenopuslib_info.shtml.
Cancer Institute of Chiid Health and Human Development, National (Dipublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR ATE_SU03_G11 adult testis subtracted 1 (TLL) Danio rerio cDNA, CO359322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.4; DB 5; Length 587; Pred. No. 3.1e+02; 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: LLAM11967 row: C column: 8
Seq primer: -21M13 forward primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AAAGATGATTAGGCAGAGGT 263
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Matches 19; Conservative
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ORGANISM
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AUTHORS
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DD
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(Liases I to 547)

Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., WashU Xenopus EST project, 1999

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Library constructed by A. Zorn and J. Mason (Wellcome/CRC
Institute). DNA Sequencing by: Washington University Genome
Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.B. Consortium/LLNL at: info@image.llnl.gov
High quality sequence stop: 507.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                             BG487106 547 bp mRNA linear EST 22-MAR-2001 dad25b04.x1 Wellcome CRC pCS107 tropicalis St10-12 Xenopus tropicalis cDNA clone IMAGE:4440511 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:4440511"
/tissue type="whole embryo, stages 10-12"
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/note="Vector: pCS107, Site_1: Not!; Site_2: EcoR!; cDNAs were oliqo-dT primed and directionally cloned. Average insert size 1.5 kb, range 0.5-4 kb. Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute). "
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BH972205 odj23910.
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WashU Kenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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Xenopus tropicalis
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/mol_type="mRNA"
/db_xref="taxon:8364"
                                                                                                                                                               ALIGNMENTS
   CN283739
CC956922
BH972205
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16
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Query Match

ORIGIN

FEATURES

Matches

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RESULT 2 BQ523985 LOCUS

ACCESSION VERSION

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Gaps

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Gaps

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EST 31-MAR-2004

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/clone libe Xenotes tropicalis xthr plasmid library"
/clone libe Xenotes tropicalis poly4. RNA was obtained from
fili, Xenopus tropicalis poly4. RNA was obtained from pool
of heads and retinas from tailbud stages 25-35 cDNAs were
synthesized using the SMART system of CLONTECH and
directionally cloned into prowysporre_xthr, a modified
version of pCWNSPORTE allowing directional cloning using
asymetric Sfil sites. For antisense RNA synthesis, use T7
promoter and for sense RNA use SP6 promoter. Library
constructed by Drs. N. Pollet, M. Perron, M. Wegnez,
Mazabraud (CNRS UMR 8080, Universite Paris Sud, Orsay,
Sfil; Xenopus tropicalis polyA+ RNA was obtained from brain and spinal cord of tadpoles at stages 51-52 and 61-62. cDNAs were synthesized using the SNART system of CLONTECH and directionally cloned into pCWNSPRT6 xtbs, a modified version of pCWNSPORT6 allowing directional cloning using asymetric Sfil sites. For antisense RNA synthesis, use 77 promoter and for sense RNA apymentels, use 77 promoter and for sense RNA apymencer. Library constructed by Dr. L. Coen and Prof. B. Demeneix (Museum National d'Histoire Naturelle and CNRS UMR 5166, Paris, France)."
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1 (bases 1 to 731)

1 (banes 1 to 731)

Shuret, R. Fierro, A.C., Porron, M., Demeneix, B., Wegnez, M. Gyapay, G., Weissenbach, J., Wincker, P., Mazabraud, A. and Pollet, N. Exploring the nervous system transcriptome in the model Xenopus Unpublished (2004)

Contact: Pollet N
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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EC2CAA16BD09.b1 Xenopus tropicalis xthr plasmid library Xenopus
tropicalis cDNA clone xthr16G18 3', mRNA sequence.
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IBAIC bat 447, Universite Paris Sud, Orsay, F-91405, Prance
Fax: +33 169157272
Fax: +33 16915618
                                                                                                                                                                                                                                                                                                                                             Query Match 92.0%; Score 18.4; DB 7; Length 689; Best Local Similarity 95.0%; Pred. No. 3.2e+02; Matches 19; Conservative 0; Mismatches 1; Indels
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    .731
    /organism="Xenopus tropicalis"

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/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="ivory coast"
/db_xref="taxon:8364"
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CN099540
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                                                                                                                                                                                                                                                    /dev stage="adult (fully mature)"
/dow stage="adult testis subtracted 1 (TLL)"
/clone_lib="adult testis subtracted 1 (TLL)"
/clone_lib="adult testis subtracted 1 (TLL)"
/note="Organ: pooled testis, Vector: pT-Advantage, cDNA
was synthesized from adult testis and ovary total RNA
using SMART PCR cDNA synthesis kit (Clontech).
PCR-SelectTM cDNA subtraction kit (Clontech) was used to
enrich for fragments, which were present in the testis but
not in the ovary cDNA. The selectively amplified cDNA
fragments (in average 400-800bp in length) were ligated
into pT-Advantage (Clontech) and transformed into
xL10-Gold competent cells (Stratagene). The insert from
randomly selected white colonies was PCR amplified using
M13 forward and reverse primers and partially sequenced by
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia, Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 689)
Thuret,R., Fierro,A.C., Coen,L., Perron,M., Demeneix,B., Wegnez,M., Gyapay,G., Weissenbach,J., Wincker,P., Mazabraud,A. and Pollet,N.
Exploring the nervous system transcriptome in the model Xenopus tropicalis using EST analysis
Unpublished (2004)
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/dev stage="stage 51-52 and 61-62"
/lab-bost=="coli bHloss"
/clone lib="Xenopus tropicalis xtbs plasmid library"
/note="Vector: pCMVSPORT6_xtbs; Site_1: Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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TBAIC Dat 447, Universite Paris Sud, Orsay, F-91405, France
TE1: +33 169157272
Fax: +33 169156816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.0%; Score 18.4; DB 7; Length 612; 95.0%; Pred. No. 3.1e+02; ive 0; Mismatches 1; Indels (
                                                                                                                                              /mol_type="mRNA"
/strain="Toh (Singaporean strain)"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kenopus tropicalis (western clawed frog)
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/mol_type="mRNA"
/strain="ivory coast"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using M13 reverse primer."
                                                                                                                       /organism="Danio rerio"
                                   High quality sequence stop: 612.
Location/Qualifiers
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/clone="xtb833N21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGAGATGATTAGGCAGAGGT 20
                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 95.0
Matches 19; Conservative
        Similar to Q9CUZ3
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CN090609
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DEFINITION

RESULT 6 CO798651

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ORGANISM

VERSION KEYWORDS SOURCE ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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BX693640

859 bp mRNA linear EST 14-NOV-2003
BX693640 XGC-neurula Xenopus tropicalis cDNA clone TNeu087h08 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/clone lib="XGC-neurula"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT prined from Sug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                   Bukarrota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

I (Dases I to 859)

Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
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Kenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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1 (bases 1 to 869)
1 (coning, M.D.R., Ashurst, J.L., Taylor, R., Garrett, N. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (2004)
Unpublished (2004)
Contact: Croning MDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
CDNA was oligo dT primed from Sug of poly A+ RNA from neurula.
ECORT-NotI cut CDNA was then ligated into pCS107 with ECORI at 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site_2: NotI
HOST: Escherichia coli DH10B.
Location/Qualifiers
1. 859
//organism="Xenopus tropicalis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Croning MDR Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Bmail: troposeanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TNeu087h08.q1kT7
Sequencing primer: T7
                                                                                                                                                                                                                                           Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                             mRNA sequence.
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AUTHORS
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CR417260
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/clone_lib=MINI ZGC_14"
/note="Organ: olfactory epithelium; Vector: pME18S-FL3;
Site=1: DraII; Site_2: DraIII; 1st strand cDNA was primed
with an oligo(dT) primer
(GGGGTGAAGACGCCTATGTGTGTGTGTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
(GGCCUACUGG), digested and directionally cloned into
(Instinct DraIII sites of the pME18S-FL3. Library was size
selected for 1.0 kb, with a average insert size of -1.2kb.
Library constructed by Yutaka Suzuki (University of Tokyo
Institute of Medical Science). Custom primers recommended
for sequencing: 5 and primer 5.-GGACTGAGGTGCGACAA-3,
and 3, and primer 5.-GGACTGAGGTGCACAA-3,
and 3, end primer 5.-CGACCTGAGCTCAACTTCTA-3
is a Zebrafish Gene Collection (ZGC) library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Educatoria, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cypriniformes, Cyprinidae, Danio.

1 (Dases 1 to 744)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
Office of Gancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bidg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John Ngai, Nancy Freeman, NIDCD
CDNA Library Preparation: Dr. Sumio Sugano
CDNA Library Preparation: Dr. Sumio Sugano
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMISS92 row: k column: 10
High quality sequence start: 4
High quality sequence stop: 624.

Location/Qualifiers

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                                                                                                                                                                                                                                                                                         CO798651 794 bp mRNA linear EST 05-AUG-2004
CENTROLOUR 30340870 NIH_ZGC_14 Danio rerio cDNA clone IMAGE:7401252
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95.0%; Pred. No. 3.2e+02;
iive 0; Mismatches 1; Indels
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/db_xref="taxon:7955"
/clone="IMAGE:7401252"
/issue_type="toffactory epithelium"
/lab_hogt="DH10B TonA"
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Danio rerio
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Best Local Similarity 95.0
Matches 19; Conservative
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CR445414.1 GI:48971001
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Best Local Similarity
Matches 19; Conserv
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AUTHORS
TITLE
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AGENCOURT_30338237 NIH_ZGC_14 Danio rerio cDNA clone IMAGE:7402168
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In Institutes of Health, Mammalian Gene Collection (MGC)

In National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm.0A07 Betheada, MD 20892

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: John Mgai, Nancy Freeman, NIDCD

CDNA Library Preparation: Dr. Sumio Sugano

CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LiNL

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov

Plate: LiAM15595 row: a column: 14

High quality sequence stop: 695.
                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from tailbud. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
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                                         Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TTDA018g16.q1kT7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
Seq primer: T7.
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/lab_host="Escherichia coli DH10B."
/clome lib="XGC-tailbud"
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/tissue type="olfactory epithelium"
/lab_host="DH10B TonA"
/clone_lib="NIH_EGC_14"
                                                                                                                                                                                                     Hinxton, Cambridgeshire, CB10 1SA, UK
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CO812154
CO812154.1 GI:51030780
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Sanger Institute
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1 (bases 1 to 896)

1 (croing, M.D.R., Ashurst, J.L., Taylor, R., Garrett, N. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (2004)
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/lab host="Escherichia coli DH10B."

/clone lib="XGC-tailbud"

/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; CDNA

/mas oligo dT primed from Sig of poly A+ RNA from tailbud.

EcoRI-NotI cut chNA was then ligated into pCS107 with

EcoRI at the 5' end and NotI at the 3' end."
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Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TrbA012n19.pikaSP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Nigel Garrett.
Seq primer: SP6.
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llarity 95.0%; Pred. No. 3.38+02;
Conservative 0; Mismatches 1; Indels
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/organism="Xenopus tropicalis"
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Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
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/db xref="taxon:8364"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

RESULT 11

BX699062

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Hinakon, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TNeu111c20.q1kT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
CDNA was oligo dT primed from Sug of poly A+ RNA from neurula.
ECORI-NotI cut cDNA was then ligated into pCS107 with ECORI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site_2: NotI
Host: Escherichia coli DH10B.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Xenopus tropicalis"
/mol type="mRNA"
/db_xref="taxon:8344"
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/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dr primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
                                           Email: trop@eanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu069h15.q1kT7
TROPICALIS_SEQUENCE_ID: TNeu069h15.q1kT7
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
ECDNA was oligo dT primed from 5.0 oppy A+ RNA from neurula.
ECONI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site_2: NotI
Host: Escherichia coli DH10B.
Location/Qualifiers
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1 (bases 1 to 914)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Contact: Croning MDR.
Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.0%; Score 18.4; DB 5; Length 913; Best Local Similarity 95.0%; Pred. No. 3.3e+02; Matches 19; Conservative 0; Mismatches 1; Indels
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/db_xref="taxon:8364"
                        Hinxton, Cambridgeshire, CB10 1SA, UK
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Sanger Institute
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BX694706
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/nofe="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNĀ from neurula.
EcoRI-NotI cut coNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end."
                                        BX699062
BX699062 XGC-neurula Xenopus tropicalis cDNA clone TNeu073a09 3',
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CDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.

ECORT.NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site_1: ECORI; Site_2: NotI

Host: Eschericina coli PH10B.

Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibla, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae; Xenopodinae, Xenopus, Silurana.
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Xenopus tropicalis

Xenopus tropicalis

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 913)

Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.

Sanger Xenopus tropicalis EST project 2001 (11_2003)
                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 910)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Kenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Croning MDR
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Hinxton, Cambridgeshire, CB10 1SA, UK
Bmail: tropedanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TNeu073a09.qlkT7
Sequencing primer: T7
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92.0%; Score 18.4; DB 5;
Best Local Similarity 95.0%; Pred. No. 3.38+02;
Matches 19; Conservative 0; Mismatches 1;
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                                                                                                      mRNA sequence.
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RESULT 12 BX683124

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REFERENCE AUTHORS

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/db_xref="taxon:10090"
/clone="IWAGE:2651190"
/clone="IWAGE:2651190"
/lab_host="DHIDB"
/lab_host="DHIDB"
/clone lib="NCI_CGAP_LU30"
/note="Organ: lung; Vector: pCWV-SPORT6; Site 1: Not1;
Site 2: Sal1; transgenic model WT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Libzary constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 bp mRNA linear EST 17-MAY-2002 CM3-CT0039-230799-001-a04 CT0039 Homo Bapiens cDNA, mRNA sequence. BQ315666 1 GI:20921435 EST.
                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDN Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 494)
1 (bases 1 to 494)
1 (bases 1. Catcin Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 384)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Pred. No. 9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -40RP from Gibco
High quality sequence stop: 3
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGAGATGATTAGGCAGAGG 19
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Best Local Similarity 94.7%;
Matches 18; Conservative (
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                                                                                                                    Tumor Gene Index
Unpublished (1997)
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                             /dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/clone_lib="XeC-neurula"
/note="Vector: pCS107; Site_l: EcoRI; Site_2: NotI; cDNA mas oligo dT primed from Sig of poly A+ RNA from neurula.
EcoRI.NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Guillardia theta Lambda Zap II cDNA Library"
/note="Vector: Lambda ZAP II; Site_1: EcoRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GthEST1 Guillardia theta Lambda Zap II cDNA Library Guillardia
theta cDNA clone 38r, mRNA sequence.
AW342249
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Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

1 (Bases I to 214)

1 (Bases I to 214)

1 (Pases I to 214)

1 (Pases I to 214)

EST Database of the cryptomonad alga: Guillardia theta

Unpublished (2000)

Contact: Maier, U.G.

Contact: Maier, U.G.

Philipps-University Marburg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karl-von-Frisch-Strasse, D-35043 Marburg, Germany
Tel: ++49 6421 282 2057
Fax: ++49 6421 282 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Guillardia theta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: maier@mailer.uni-marburg.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:55529"
       /clone="TNeu111c20"
                                                                                                                                                                                                                                                                                                                                                              245 AAAGATGATTAGGCAGAGGT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="CCMP327"
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Mus musculus (house mouse)
Mus musculus
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/lab_host="SOLR"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [ Léase] 1 to 71]

Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSS: RPCI-24-273E14.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
             /lab host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_l: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao¢tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library APCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC e
page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                   Length 680;
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RPCI-24-273E14.TJ RPCI-24 Mus musculus genomic clone
RPCI-24-273E14, genomic survey sequence.
                                                                                                                                                                                                 1; Indels
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                              ch 87.0%; Score 17.4; DB 4; 1 Similarity 94.7%; Pred. No. 9.9e+02; 18; Conservative 0; Mismatches 1;
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/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="RPCI-24-273E14"
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Mus musculus
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                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0039"
/note="Organ: colon; Vector: pucl8; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-CT0039-230799-001-a04&t3=1999-07-23&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence start: 14
High quality sequence stop: 139.
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Gossypium arboreum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
I cosids; eurosida II, Malvales; Malvaceae, Malvoideae, Gossypium.
I (bases 1 to 680)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="8400"
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/clone="GA_E0005K32f"
/tissue_type="Fibers isolated from bolls harvested 7-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.0%; Score 17.4; DB 5; Length 494; 94.7%; Pred. No. 9.4e+02; live 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Gossypium arboreum"
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Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 600.
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Matches 18, Conservative
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BG440037/c
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Gaps

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BB361792 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130006N13 3' similar to X76772 M.musculus mRNA for ribosomal protein S3, mRNA sequence.
BB361792. GI:9073620
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Submitted (12-ARR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 248)
1 (bases I to 248)
Carninci, P., Alzawa, K., Akahira, S., Rukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Ishikawa, T., Ishikawa, T., Ishikawa, T., Ishikawa, T., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyoswa, H., Kolina, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
                      Tetraodon nigroviridis
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="G"
/note="Genoscope sequence ID : COAG243AC06LP1~end : T7"
                                                                                                                                                                                                                                                Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000) 10835643
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/db_xref="taxon:99883"
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Pred. No. 1.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGAGATGATTAGGCAGAGG 19
Tetraodon nigroviridis
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr and and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                CNS029UK 1032 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 249Bl3 of library G from Tetraodon nigroviridis, genomic survey
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GGS; genome survey sequence.
GGS; genome nigroviridis
Tetracdon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Teleostei; Neoteleostei;
Acauthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracontoidea; Tetracodontidae; Tetracodon.
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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94.7%; Pred. No. 1.1e+03;
iive 0; Mismatches 1;
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AL184764.1 GI:7822868
GSS; genome survey sequence.
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/clone_lib="G"
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Best Local Similarity 94...,
Thes 18; Conservative
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CNS027K3/c
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CNS029UK
LOCUS
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PUBMED REFERENCE AUTHORS JOURNAL MEDLINE

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REFERENCE AUTHORS

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FEATURES

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COMMENT

PUBMED JOURNAL MEDLINE

ACCESSION VERSION KEYWORDS

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Gapa

TITLE JOURNAL COMMENT

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1 (bases 1 to 490)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                  AQ355954 110-232A22.TR CITBI-E1 Homo sapiens genomic clone 2532A22,
                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Other GSSs: CITBI-B1-2532A22.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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1 (Bases I to 145)

Dias Neto. B. (Barcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF330446 12-NOV-2000 MR2-BN0364-220800-012-b01 BN0364 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                           Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="sperm"
/clone_lib="CITBI-El"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%; Score 17; DB 8; Length 490;
100.0%; Pred. No. 1.5e+03;
.ive 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                 genomic survey sequence.
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                                                                                                                                              AQ355954.1 GI:4183127
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108 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome_res@gec.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci.P., Nishiyama.Y., Westover.A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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Itoh,M., Kitsunai,T., Akipama,J., Shibata,K., Izawa,M., Kawai,J.,
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System. Genome Res. 9 (5), 463-470 (1999)
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Suzuki,H., Tagawa,A., Sogabe,Y., Sugahara,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Towinod,Y., Watahiki,A., Watahiki,A., Yokota,Y., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,Y., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y., Yoshino,M., Muramatsu,M. and RIKEN Wouse ESTS (Konno,H., et al.)

L. Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC). Yokohama Institute Sciences Center (GSC). Yokohama Institute
Sciences Center (GSC). Yokohama and Chemical Research (RIKEN)
1-7-2 Sushino-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="RIKEN full-length enriched, 16 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="head"
/dev stage="16 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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source

FEATURES

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Gaps ö Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

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/mol_trpe="manna" or provided by the products of the provided from the provided by the products of the provided by the products of the provided by the provide
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S Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
Katzenburger, F., King, L., Miller, S., Muller, S., Nascimento, L.,
Zutavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
Unpublished (2002)
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8874
Email: mccombie@cshl.org
Plate: hts8 row: d column: 07
Seq primer: 21M13UnivRev
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                            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR2&t2=MR2-BN0364-280800-010-b02&t3=2000-08-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 146.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 16.8; DB 2; Length 146; 90.0%; Pred. No. 1.6e+03; ive 0; Mismatches 2; Indels (
   This entry can be seen in the following URL
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                                                                                                                                                                                                                                         /organism="Homo sapiens"
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Location/Qualifiers
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Sorghum bicolor
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nes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Bases I to 146)
Dias Neto, E. García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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MR2-BN0364-280800-010-b02 BN0364 Homo sapiens cDNA, mRNA sequence.
BF330451
                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-BN0364-
220800-012-b01&t3=20000-08-22&t4=1)
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This sequence was derived from the PAPESP/LICR Human Cancer Genome
                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
abboratory of Cancer Genetics.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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90.0%; Pred. No. 1.6e+03;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: puc 18 forward
High quality sequence stop: 145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Fax: +55-11-2707001
                                                                                                                                                                                                                                      rel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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BF330451
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Email: cgapbs-remail.nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
Tissue Procurement: David G. Bostwick, M.D., Rh.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 318 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AJ572696 AM3/RH2 Homo sapiens cDNA clone HSPD45782, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="prostate"
|/tlab_host="DHIOB"
|/ab_host="DHIOB"
|/clone_lib="NUI_CGAP_pr8"
|/note="Vector: pAMPl0; mRNA made from invasive prostate fumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
Laveder, P., De Pitta, C., Vitulo, N., Valle, G. and Lanfranchi, G.
Oligo-directed RNase H cleavage of abundant mRNAs in skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Via U. Bassi 56/B. 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW http://muscle.cribi.unipd.it
BIOLIMS code: sHr-000004-0-H07
Seq primer: PC2R.
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/clone_lib="HM3/RH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%; Score 16.8; DB 1; Length 407; 90.0%; Pred. No. 1.8e+03; ive 0; Mismatches 2; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSPD45782"
                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:956706"
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Contact: Laveder P
CRIBI Biotechnology Centre
University of Padua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 AGAGAAGATGAGGCAGAGGT 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
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Matches 18; Conservative
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AJ572696
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AUTHORS
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kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."
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                                                                                                                                                                                                                                                                                                                                                                                           AJ713073 LKPD01 Homo sapiens cDNA clone LKPD01049, mRNA sequence.
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1 (bases 1 to 388)
DePitta, C., Tombolan, L., Kronnie, G., Romualdi, C., Vitulo, N., Basso, G. and Lanfranchi, G.
Alenkemia-enriched cDNA microarray platform identified new transcripts with relevance to the biology of leukemias Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA503497 10-2 CGAP_Pr8 Homo sapiens cDNA clone IMAGE:956706 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 407)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                               Gaps
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                                                                                                                       Score 16.8; DB 8; Length 387;
Pred. No. 1.8e+03;
0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue type="bone marrow"
/clone_lib="LKPD01"
/note="caucasian"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Depite C
Biology and CRIBI
University of Padova
Via U. Bassi, 58/8, 35131, ITALY.
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/db_xref="taxon:9606"
/clone="LKPD01049"
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AA503497
AA503497.1 GI:2238464
                                                                                                                     Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
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Homo sapiens
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Matches 18; Conservative
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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VERSION KEYWORDS SOURCE ORGANISM

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RESULT 27

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E 1 (bases 1 to 506)

S Clark, M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Bddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Kiter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998

L Ontact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 484)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Aonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A. Bincet, Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
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                                                                                                                                                                                                                        BX975154 linear GSS 05-JUL-2004 Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP76122, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE558110
506 bp mRNA linear EST 30-AUG-200 [119f03.yt Zebrafish Research Genetics C32 fin Danio rerio cDNA 5' similar to TR:015249 015149 PDZ DOMAIN PROTEIN. [2] TR:060833 ;contains element TAR1 repetitive element ; mRNA sequence.
                                            Gaps
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0
Length 423;
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      1.8e+03;
84.0%; Score 16.8; DB 1;
90.0%; Pred. No. 1.8e+03;
tive 0; Mismatches 2;
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BX975154.1 GI:49706577
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="WHPP76122"
/clone_lib="MHPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 AGAGATGATTAGGAAGAGT 213
                                                                               1 AGAGATGATTAGGCAGAGGT 20
                                                                                                           75 AGAAATGATGAGGCAGAGGT 94
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Danio rerio
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                                          18; Conservative
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. 1 (bases 1 to 509)

E Junn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Roos, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

L Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone lib="Zebrafish Research Genetics C32 fin"
// note="Vector: pT71D-Pac with a modified polylinker;
Site_1: ScoRi, Site_2: NotI; lst strand cDNA was prepared
from Zebrafish (G32) fin, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is non-normalized. Library was
constructed by Ning Wu. NOTE: This clone is available
royalty-free through LiNL; contact the IMAGE Consortium
(info.llnl:gov) for further information"
                          cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
Research Genetics. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Research Genetics web
address: http://www.researchgenetics.com/
Seq primer: T3 ET from Amersham
High quality sequence stop: 470.
                                                                                                                                                                                                                                                                                                                                                                                                                                        /tisaue_type="Fin"
/lab host="GeneHogs (HS996, a phage-resistant isolate of
DH10B)"
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Insert Length: 10000 Std Brror: 0.00
Plate: 0066 row: A column: 09
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:7955"
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nes 18; Conservative
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Fax: 801 585 7177
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source

organism="Homo"

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DEFINITION
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KEYWORDS
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CB719936
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BE605742
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                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
[http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwb22 (gi|4732114|gb|AR129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli Xi10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
E Hobses 1 to 525)
B Adame, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Other GSss RPCIII-79113. TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomics Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 1018 389 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV31/545
RPCIII-79113.TJC RPCI-11 Homo sapiens genomic clone RPCI-11-79113,
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                                                                                                                      /lab host="E. Coli strain Xil0-Gold, Ti-resistant, F-" /clone_lib="Mouse_10kb plasmid_UUGCIM library" /note="Vector: PWD42nv; Purified genomic_DNA from M.musculus_C57BL/60 (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

Seq primer: SP6

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%; Score 16.8; DB 8; Length 509; 90.0%; Pred. No. 1.9e+03; .ive 0; Mismatches 2; Indels (
'mol_type="genomic DNA"
'strain="C57BL/6J"
                                             db_xref="taxon:10090"
clone="UUGC1M0066A09"
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Location/Qualifiers

FEATURES

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AMGNNUC:NRDG1-00073-C10-A nrdg1 (10855) Rattus norvegicus CDNA
Clone nrdg1-00073-C10 5', mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                                                                                                                                                                                                                                                                             /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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    .526
    /organism="Rattus norvegicus"

/mol_trpe="genomic DNA"
db_xref="dDB:75,0156"
/db_xref="taxon:9606"
/clone="RPCI-11-79113"
/sex="Male"
                                                                                                                                                                                                                                     /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
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Location/Qualifiers
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Rattus norvegicus
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Contact: Dan Fitzpatrick
Amgen, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB719936.1 GI:29777078
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Amgen EST Program.
Amgen Rat EST Program
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Best Local Similarity 90.03
Matches 18; Conservative
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VERSION
KEYWORDS
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ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

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/clone lib="MGLSD"
/note="Vector: pBluescript SK-; Site_1: ECORI; Site_2:
Xhot; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. CDNA was prepared from polyA+ enriched RNA.
The CDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Giappack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         537 bp mRNA linear EST 24-FEB-2004 eca01-43mg3-f11 Eca01 Eschscholzia californica cDNA clone eca01-43mg3-f11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eschecholzia californica (California poppy)

Bschscholzia californica

Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Wagnoliophyta; eudicotyledons; Ranunculales;

Papaveraceae; Eschscholzioideae; Eschscholzia.

1 (Dases I to 537)

dePamphilis,C., Carlson,J., Ma,H., Tanksley,S., Field,D.,
Leebens-Mack,J., Arrington,J., Zahn,L.M., Kong,H., Ilut,D.,
Druckenmiller,M., Landherr,L., Hu,Y., Plock,S., Wall,K.,
Chiorean,S., Albert,V., Doyle,J., Frohlich,M., Miller,W.,
Oppenheimer,D., Soltis,D., Soltis,P. and Theiseen,G.
Generation of ESTB from early flower buds of Eschscholzia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
                                                                                                                                                                                                                                                                                        Email: mgrusak@bcm.tmc.edu
TIGR sequence name: MTRAD82TK More information is available at:
Cheung, F. and Fraser, C.M.

BSTs from late stage developing seeds of Medicago truncatula Unpublished (2002)
Contact: Grusak, M.A.

USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3880"
/clone="pGLSD-28N30"
/tissue_type="Immature seeds"
/dev erage="25 to 35 days after pollination"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 533;
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Mueller Laboratory
                                                                                                                                                                                                                                                                                                                                                www.medicago.org
Seg primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
/mol type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 AGAGATGATGAGGCAGAGTT 403
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                                                                                                                                                                                                                      Tel: 713 798 7044
Fax: 713 798 7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
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Best Local Similarity
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JOURNAL
COMMENT
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CK766395
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KEYWORDS
SOURCE
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                                                    Eddy, S. Haraca, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi;
Cypriniformes, Cyprinidae, Danio.
I (Janes 1 to 531)
S clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kacaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, R., Theising, B., Allen, M., McCann, R., Washu Zebrafish Est Project 1998
Unpublished (1998)
Unpublished (1998)
Contact: Stephen L. Johnson Kashington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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EST607999 GLSD Medicago truncatula cDNA clone pGLSD-28N20, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone lib="zebrafish Research Genetics C12 fin"
//note="Vector: pT713D-Pac with a modified polylinker;
Site_1: ECORI; Site_2: NotI; lst strand cDNA was prepared
from zebrafish (C12) fin, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
ECO RI adaptors (Pharmacia), digested with Not I and
Cloned into the Not I and ECO RI sites of the modified
pT7T3 vector. Library is non-normalized. Library was
constructed by Ning Wu. NOTE: This clone is available
royalty-free through LiML; contact the IMAGE Consortium
(info.llnl.gov) for further information"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Medicago truncatula
Subraryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosida, eurosida I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Fin"
/lab_host="GeneHogs (HS996, a phage-resistant isolate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
Research Genetics. DNA Sequencing by: Washington University
Sequencing Center Clone distribution: Research Genetics web
address: http://www.researchgenetics.com/
Seq primer: T7 Fr from Amersham
High quality sequence stop: 426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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90.0%; Pred. No. 1.9e+03;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:7955"
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BQ122423.1 GI:20174385
      Danio rerio (zebrafish)
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Matches 18; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

ACCESSION

RESULT 35

DRIGIN

BQ122423

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Gaps

FEATURES

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Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: SP6
Class: BAC ends.
                                              (http://bacpac.med.buffalo.edu/ordering) or from (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please context Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@reegen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 568)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of BAC Bnd Sequences from Library RPCI-11 for Sequence-Ready Map Building Unpublished (1997) Cher GSSs: RPCI-11-381N22.TJ Coher GSSs: RPCI-11-381N22.TJ Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male" | color | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: BcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPCI-11-381N22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-381N22, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 16.8; DB 8; Length 90.0%; Pred. No. 1.9e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic_DNA"
/db_xref="GDB:7594384"
/db_xref="taxon:9606"
/clone="RPCI-11-246M17"
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1. :568
/organism="Homo sapiens"
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/db_xref="GDB:7646253"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                Location/Qualifiers
1. 558
/organism="Homo sapi
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AQ554673.1 GI:4913850
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Best Local Similarity
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AQ554673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db xref="texton:3467"
/clone="eca01-4]ms3-fil"
/tissue_type="flower buds <= 2.5mm"
/tissue_type="flower buds"
/lab host="SOLR"
/lab host="SOLR"
/clone]lib="BEca01"
/note="Vector: pBluescript SK (+/-); Site 1: ECORI;
/site 2: Xho1; Plants were grown in greenhouse at Penn Site 2: Xho1; Plants were grown in greenhouse at Penn State from commercially available seeds. Only floral buds with diameter of 2.5 mm of less were collected. This is a directionally cloned, non-normalized library. Avg. insert length: 1702; Primers: Milf and Milfied This is a directionally cloned, non-normalized library. Avg. insert length: 1702; Primers: The pfu total; Amplified Titer: 1.68B1 pfu/ml; Mass Exclsed Titer: 5.6B8 total; This library has been generated by the Floral Genome Project (FGP). We would like to thank Huck Life Sciences Consortium for their assistance. The Floral Genome Project is funded by NBF's Plant Genome Research Program (BBI-0115684). More information about the project can be obtained at http://fgp.bio.psu.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E. 1 (Beases It o. 558)

S. Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Use of BAC BAC Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)

L. Onpublished (1997)

L. Onpublished (1997)

L. Onpublished (1997)

L. Onpublished (1997)

The Institute for Genomics Research
9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Tel: 301 838 0200

Tel: 301 838 0200

Tel: 301 838 0200

Tel: And Man Secure de Jong

Clones are derived from the human BAC library RPCI-11. For BAC library availability please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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State University, University Park, PA 16802, USA Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhll0@psu.edu
The sequence provided is trimmed of vector and low qrell sequence and original trace file are available fornome Network website (http://pgn.cornell.edu)
Plate: eca01-43ms3 row: f column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 537;
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RPCI-11-246M17, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Eschscholzia californica"
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84.0%; Score 16.8; DB 7;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Aurantiaca Orange"
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AQ491131

RESULT 37 AQ491131 LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE Ношо

ORGANISM

REFERENCE

AUTHORS

JOURNAL TITLE

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Gaps

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GSS 28-MAY-1999

ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

FEATURES

DEFINITION

ACCESSION

RESULT 39 BJ690447

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Inote="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, def-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B00642 627 bp DNA linear GSS 13-JUL-1996 CSRL-117e7-u CSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-117e7, genomic survey sequence.
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1 (bases 1 to 627)
Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Jones, D., Mard, T., Gillilan, E., Schagemann, J., Probet, S., Khan, M., Kupfer, K., and Garner, H. R., Chan, M., Kupfer, K., and Garner, H. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Sorghum methylation-filtered library (LibID: 104)"
Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J., Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A. Generhresher methylation filtered genomic sequences from Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 214-648-1666
Email: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 16.8; DB 9; Length 614; 90.0%; Pred. No. 1.9e+03; ive 0; Mismatches 2; Indels (
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McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At
5323 Harry Hines Blvd, Dallas TX 75235-8591
                                                                                                  Unpublished (2004)
Contact: Bedell JA
Contact: Bedell JA
Cortion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 401 row: c column: 18
Seq primer: T3 Reverse
Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                1. .614
/organism="Sorghum bicolor"
/mol type="genomic DNA"
/cultivar="ATx623"
/db xref="texon:4558"
/clone="10900146"
                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 614.
Location/Qualifiers
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BACKWARD: GCATTGTGAGTTGGTTAGTC
Seq primer: I7
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Haplochropis (Tanidata) (Tanidata) (Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidei; Cichlidae; Haplochromis.

El (bases 1 to 599)
Watanabe, M., Kobayashi, N., Shin-i, T., Kohara, Y. and Okada, N.
Orf sequences of cichlid in Lake Victoria are essentially same
Lumpublished (2004)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                           BJ690447 BJ690447 HREST library Haplochromis sp. 'red tail sheller' cDNA clone no589h05, mRNA sequence.
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1 (Dasse 1 to 614)

Budiman, M.A., Flick, E., Jones, J., Numberg, A., Citek, R.W.,
                                                                                                                                    Gaps
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                            Query Match 84.0%; Score 16.8; DB 8; Best Local Similarity 90.0%; Pred. No. 1.9e+03; Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%; Score 16.8; DB 4;
90.0%; Pred. No. 1.9e+03;
tive 0; Mismatches 2;
RPCI11 Human Male BAC Library"
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/clone_lib="HREST library"
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/db_xref="taxon:257976"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Matches 18; Conservative
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Query Match

ORIGIN

CL186343/c LOCUS DEFINITION

RESULT 40

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION

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Gape

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Contact: Richard K. Wilson
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odh59 row: a column: 02
Seq primer: -28RPpOT reverse
                                                                                                                                                                                                                                                            Score 16.8; DB 6
Pred. No. 2e+03;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 49
High quality sequence stop: 535.
Location/Qualifiers
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Sequencing Center."
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Best Local Similarity 90.0%;
Matches 18; Conservative (
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BH975438
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above BST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA
Clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                        /note="Vector: sCos-1; Human Chromosome 11 specific cosmid
library prepared from flow sorted human Chromosome 11
derived from Chinese Hampster Ovary (CHO) monochromosomal
somatic cell hybrid, J1"
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BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
High quality sequence stop: 663.
Location/Qualifiers
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                                                                                                                                         /cell_type="chimeric hamster somatic cell hybrid" /clone lib="cSRL flow sorted Chromosome 11 specific cosmid"
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StrPu691.001255 Sea urchin larva cDNA library MPMGp691
                                                                                                                                                                                                                                                                                                                                    84.0%; Score 16.8; DB 8; Length 627; 90.0%; Pred. No. 1.9e+03; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                               2; Indels

    .663
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus purpuratus cDNA clone
MPMGp691C0520;MPI_SURUDI_20C5 5', mRNA sequence.
                                           'organism="Homo sapiens"
                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus
Location/Qualifiers
                                                                                                      /clone="cSRL-117e7"
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                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
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Matches 18; Conserva
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/tissue_type="whole larva"
/tissue_type="whole larva"
/tissue_type="whole larva"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH975438 699 bp DNA linear GSS 02-OCT-2002 odh59a02.91 B.oleracea002 Brassica oleracea genomic, genomic survey
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Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Whole genome showicz,P.D. and Wilson,R.K.
Whole genome shoughn reads from Brassica oleracea
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/db xref="taxon:3712"
/clone lib="B.oleracea002"
/note="vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
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Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Genil: schaochigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
This BAC end was generated during the R&D process and may have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Jesue L'Equato.
// Jesue L'Eduating, Neonatal"
// Jab_host="DH10B TonA"
// Jab_host="DH10B TonA"
// Johne lib="BAKE BBOV"
// Johne lib="BBOV"
// John
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                                                    Email: Tbaumanneanri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.00025 using options -trim_alt '. -trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
Plate: 42 row: M column: 11
Seq primer: CCTATTAGGTGACCTATAGAAC
High quality sequence stops: 716.
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Unpublished (1997)
Other_GSSs: RPCI11-79II3.TJC RPCI11-79II3.TV
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/sex="Female"
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AZ519049.1 GI:10830166
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Matches 18; Conserv
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                               BH973998 10-CT-2002 OMA linear GSS 02-OCT-2002 odh10c03.bl B.oleracea002 Brassica oleracea genomic, genomic survey
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4126207 BARC 8BOV Bos taurus CDNA Clone 8BOV_42M11 5', mRNA
                                                                                                                                                                                                                                                              Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.
Construction and Analysis of a CDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Unpublished (2004)
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
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90.0%; Pred. No. 2e+03;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: column: 03
Seq primer: -21UPpOT forward
Class: shotgun
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High quality sequence stop: 551.
Location/Qualifiers
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Bovine Functional Genomics Lab
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                               Brassica oleracea
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CN791475/c
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KEYWORDS
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ORGANISM
BH973998/c
                                                       DEFINITION
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AUTHORS
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CL189821/c
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Rattus norvegicus cDNA clone
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/tissue type="Mixed tissues"
/dev_stage="Adult"
/lab_host="DHUBE (Life Technologies) (Tl phage resistant)"
/lab_host="DHUBE (Life Technologies) (Tl phage resistant)"
/clone_lib="NCI_CGAP_FF0"
/note="Vector: pTyT3-Pac (Pharmacia) with a modified
polylinker; Site_l: BcoR I; Site_2: Not I; UI_R-FF0 is a
subtracted cDNA library containing the following
tissue(s): Normal cartilage and SR-UWS Tumor Line . The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 315 8250 Fax: 319 335 9565
Fax: 310 9665
Fax: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 729)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                   /cell type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%; Score 16.8; DB 8; 90.0%; Pred. No. 2e+03; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ782214
UI-R-FF0-cpj-o-14-0-UI.sl NCI CGAP_FF0 Rs
BQ782214
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/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                       1. .718
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                       /mol_type="genomic_DNA'
/db_xref="GDB:7530156"
                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="RPCI-11-79113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
Rattus norvegicus
                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                              sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
Class: BAC ends
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Best Local Similarity
Matches 18; Conserv
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TITLE
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                                                                                                18
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
[bases 1 to 734]
Budiman, Ma., Filick,E., Jones,J., Nunberg,A., Citek,R.W.,
Robbins,D., Rohlfing,T., Bradford,K., Fries,J., MoMenamy,J.,
Trani,L., Isak,A., Zimmerman,C., Lakey,N. and Bedell,J.A.
GeneThresher methylation filtered genomic sequences from Sorghum
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Subtraction was made according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The oligonucleotide used to prime the synthesis of first-strand conds contains a library tag sequence that i located between the Not I site and the (dr)18 tail. The sequence tags for these libraries are: CTAATGGACG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'clone_lib="Sorghum methylation-filtered library (LibID:
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0
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Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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Unpublished (2004)
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@criongenomics.com
                                                                                                                                                                        CATTCTTGTA.
TAG TISSUE=rat SRC-JWST tumor line
TAG_LIB=UI-R-FF0
                                                                                                                                                                                                                                                                                                                                                   Query Match

84.0%; Score 16.8; DB 5;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2;
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High quality sequence stop: 734.
Location/Qualifiers
1. 734
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
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Seq primer: M13/pUC Forward
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/clone="10905649"
                                                                                                                                                                                                                                                                  FAG_SEQ=CATTCTTGTA"
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REFERENCE
AUTHORS
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JOURNAL
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/clone_lib="WGS-SbicolorF (JM107 adapted methyl filtered)"
/clone_lib="WGS-SbicolorF (JM107 adapted methyl filtered)"
/note="Sitte 1: Xba I; Site_2: Xba I; The vector was
digested with XbaI and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (:x/y reads in M13mp19,
.b/g reads in DU019). The same ligation was transformed in
either JM107 or DH5a."
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Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP113b19, genomic survey sequence. CR100681.1 GI:49848081
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus (bouse mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                      DNA linear GSS 12-NOV-2002 adapted methyl filtered) Sorghum
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                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 746)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Catavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A.
Genomic Shotgun sequences from Sorghum bicolor (methyl-filtered) Unpublished (2002)
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hs87c01.bl WGS-SbicolorF (JM107 adapted methyl filtered) S
bicolor genomic clone hs87c01 5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Fax: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="h887c01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 746.
Location/Qualifiers
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Plate: h887 row: c column: 01
Seq primer: -21Ml3UnivFwd
Class: shotgun
                           159 AGAGATGATTAGACAGATGT 140
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1 AGAGATGATTAGGCAGAGGT 20
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REFERENCE 1 (Dases 1 to 751)
AUTHORS Addms, D. 1. Biggs, P. 1. Cox, A. V. Davies, R. W., van der Weyden, L., John Chare, J. 1819s, P. 1. Cox, A. V. Davies, R. W., van der Weyden, L., John Chare, J. 1819s, P. 1. Cox, A. V. Taylor, R. Wishliama, L. Yu, Y. P. 1. Society, J. Plank, R. W., Taylor, R. Wishliama, T. Yu, Y. P. 1. Cox, A. Cox, Mahliama, T. Yu, Y. P. 1. Cox, M. Cox, Mahliama, T. Yu, Y. P. 1. Cox, M. Cox,
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          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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PAT 29-SEP-1999

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Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
Mills, J.S.
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Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and
Mills, J.S.
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Location/Qualifiers
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Patent: US 5856459-A 38 05-JAN-1999;
Location/Qualifiers
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Sequence 38 from patent US 5856459.
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Sequence 8 from patent US 5856459.
AR027810
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Sequence 4 from Patent W00138498.
AXIS1115
AXIS1115.1 GI:14533317
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AX151115/C
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AF528284 Hepatitis
AF528286 Hepatitis
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AF528298 Hepatitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weindel, K., Riedling, M. and Geiger, A.
Magnetic glass particles, method for their preparation and uses
thereof
Patent: WO 0137291-A 18 25-MAY-2001;
Roche Diagnostics GmbH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="derivatization with a p-(t-butyl)benzyl-residue"
/mod_base=OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                              Unknown.
Unclassified.
1 (bases 1 to 20)
Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J.Charles. and Mills, J.S.
Oligonucleotides specific for hepatitis B virus
Patent: US 5856459-A 7 05-JAN-1999;
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                  Sequence 7 from patent US 5856459.
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Sequence 18 from Patent W00137291.
AX147024.1 GI:14346295
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synthetic construct
artificial sequences.
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Best Local Similarity 85.0°
Matches 17; Conservative
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PAT 29-SEP-1999

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PAT 22-JUN-2001

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/note="Base substitution has occurred at this position in
                                                                                                                                                                                                                                                                                                                                      /note="Base substitution has occurred at this position in E2 and WO(wild-type)"
                                                                   'note="Base substitution has occurred at this position in
                                                                                                                                                         occurred at this position in
                                                                                                                                                                                                                                                'note="Base substitution has occurred at this position in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPBPRECA 99 bp DNA linear VRL 11-MAY-199
Hepatitis B virus typel precore protein (pre-C region, C) gene, 5'
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M76687.1 GI:485341
e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (baees 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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mol_type="genomic DNA"
db_xref="taxon:10407"
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                                                                                                                                                         note="Base substitution has
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85.0%; Pred. No. 16;
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                                                  'gene="pre-C/C"
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/gene="C"
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/gene="C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="pre-C/C"
/note="Base substitution has occurred at this position in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 9)
Galibert, F., Mandart, E., Fitoussi, F., Tiollais, P. and Charnay, P.
Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
cloned in B. coli
Nature 281 (5733), 646-650 (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li,J., Tong,S., Vitvitski,L., Zoulim,F. and Trepo,C.
Rapid detection and further characterization of infection with hepatitis B virus variants containing a stop codon in the distal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPBPRECAA 93 bp DNA linear VRL 24-JAN
Hepatitis B virus variant B3 genomic RNA, entire pre-C region.
D30625 D01192
D30625.1 G1:484048
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                   Stuyver, L., Schinazi, R., de Gendt, S., van Geyt, C., Zoulim, F., Fried, M. and Rossau, R. A new genotype of hepatitis b virus Patent: WO 0138498 4 31-MAY-2001; Pharmasset, Inc. (US); INNOGENETICS N.V. (BE) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="HBeAg-negative HBV variant B3~pre-C region"
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/protein id="BAA6312.1"
/b_xref="G1:507810"
/ramslation="MQLFHLCLIISCTCPTFQASKLCLGWLWGMD"
                                                                                                                                                                                                                                                                                      Length 87;
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7. Gen. Virol. 71 (Pt 9), 1993-1998 (1990)
91011344
2212990

    .87
    ^arganism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"

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    . 93
/organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db_xref="taxon:10407"

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gene="pre-C/C"
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/codon_start=1
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                  synthetic construct artificial sequences.
 synthetic construct
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    .99
    /organism="Hepatitis B virus"
/mol_type="genomic DNA"

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/gene="C"
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HPBPRECD/c
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KEYWORDS
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            /gene="C"
/note="g in wt; a in virus type 1 (creates internal stop
codon)"
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                                                                                                                                                                                                                                                                                                     W76688.1 GI:485343
e antigen; precore protein; tolerogen.
Hepatitit B virus
Hepatitit B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (baess 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                      Gaps
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Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
1853582
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                                                                                       DB 14; Length 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Frandard_name="pre-C region"
/codon_start=1
/codon_strecore protein"
/protein_id="AAAA4508.1"
/db_xref="GI:485344"
/cranslation="MQLFHLCLISCSCPTVQASKLCLGWL"
                                                                                                                    0; Indels
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Location/Qualifiers
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/organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db_xref="taxon:10407"
                                                                                  Query Match 100.0%; Score 20; DB Best Local Similarity 85.0%; Pred. No. 16; Matches 17; Conservative 3; Mismatches
                                                                                                                                                              42 AGAGATGATTAGGCAGAGGT 23
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/gene="C"
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/gene="C"
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HPBPRECB/c
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HPBPRECC/c
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DEFINITION
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/note="g in wt; a in virus type 3 (creates internal stop
codon)"
e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and Will, H.
Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area virology 183 (2), 840-844 (1991)
                                                                                                                                                                                          Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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Location/Qualifiers
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/organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db_rref="taxon:10407"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard_name="pre-C region"
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100.0%; Score 20; DE
Best Local Similarity 85.0%; Pred. No. 16;
Matches 17; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
product="precore protein"
protein_id="AAA45509.1"
db_xref="G1:485346"
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HPBPRECF 99 bp DNA linear VRL 11-MAY-1994 Hepatitis B virus type 6 precore protein (pre-C region, C) gene, 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="C"
/note="t in wt; c in virus type 6 (loss of start codon)"
                                                                                                                                                                                                                                                                                 e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and
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1853582
                                     Gaps
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100.0%; Score 20; DB 14; Length 99;
85.0%; Pred. No. 16;
ive 3; Mismatches 0; Indels
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Location/Qualifiers
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/mol type="genomic DNA"
/db xref="taxon:10407"
10. 99
/gene="C"
10. 99
/gene="C"
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Hepatitis B virus
Hepatitis B virus
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85.0%; Pred. No. 16;
tive 3; Mismatches
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/note="putative cds"
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M76692.1 GI:485351
                                     17; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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HPBPRECG/c
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                                                                                                                                                                                                                             /note="g in wt; a in virus type 4 (creates internal stop codon)"
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e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis P virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
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                                                                                                        /codon_start=1
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/db_xref="GI:485348"
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Location/Qualifiers
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/mol_type="ganomic DNA"
/db_xref="taxon:10407"
10. 93
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product="precore protein"
protein_id="AAA45511.1"
db_xref="G1:485350"
   'db_xref="taxon:10407"
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/gene="C"
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/gene="C"
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Best Local Similarity 85.09
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/note="g in wt; a in virus type 7 ( creates internal stop
codon)"
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/note="a in wt; t in virus type 7 (loss of start codon)"
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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/db_xref="caxon:10407"
/gene="C"
/gene="C"
/product="precore protein"
/grandard_name="pre-C region note: putative CDS"
                                                                                                                                                                                                                                                     /gene="C"
/note="a in wt; g in virus type 7 (gln to arg)"
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|standard_name="pre-C region note: putative CDS"
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source text: Hepatitis B virus DNA.
Location/Qualifiers
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/db_xref="taxon:10407"
10. 93
/gene="C"
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/gene="C"
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M76694.1 GI:485353
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HPBPRECH/c
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Hepatitis B virus type 11 precore protein (pre-C region, C) gene, 5, end.
M76697
M76697
e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
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M76695.1 GI:485354
e antigon, precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and Will,H.
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/gene="C"
/product="precore protein"
/standard_name="pre-C region note: putative CDS"
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|mol_type="genomic DNA"
|dD_xref="taxon:10407"
|10.93
100.0%; Score 20; DB
85.0%; Pred. No. 16;
tive 3; Mismatches
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/note="g in v
codon)"
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M76699
M76699.1 GI:485361
                                                                     'gene="C"
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           /note="frameshift mutation, deletion of single base in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e antigen; precore protein; tolerogen.
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G., Pape,G.R. and Will,H.
                                             Prevalence and type of pre-C HBV mutants in anti-HBe positive carriers with chronic liver disease in a highly endemic area Virology 183 (2), 840-844 (1991)
91306476
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                                                                                                                                                                                                                                                                    /product="precore protein"
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db_xref==GI:485583."
/translation="MQLPHLCLIISVHVILPKPPSCALGGFGTW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 14; Length 99;
85.0%; Pred. No. 16;
tive 3; Mismatches 0; Indels
             1 (bases 1 to 99)
Santantonio,T., Jung,M.C., Miska,S., Pastore,G.,
                                                                                                                             Original source text: Hepatitis B virus DNA.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10407"
10..99
/gene="C"
/gene="C"
                                                                                                                                                               /organism="Hepatitis B virus"
/mol_type="genomic DNA"
/db xref="taxon:10407"
10. 99
/gene="C"
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/gene="C"
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Best Local Similarity 85.01
Matches 17; Conservative
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                                                                                                                                                                                                                                                             gene="C
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                                                                                                                                                                                                                                                                                                                                      /gene="C"
/note="g in wt position 94; a in virus type 12 position
93"
                                                                                                                                                                                                                                                             note="t in wt position 91; a in virus type 12 position
                                                                                                                                                         note="frameshift mutation, deletion of single base in
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases I to 99)
Santantonio, T., Jung, M.C., Miska, S., Pastore, G., Pape, G.R. and
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product="precore protein"
protein_id="AAA4514.1"
db_xref="G1:485360"
'translation="MQLFHLCLIISVHVLLFKPPSCALGGFRTW"
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Location/Qualifiers
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/db_xref="taxon:10407"
10. .99
/gene="C"
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/gene="C"
/standard_name="pre-C region"
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100.0%; Score 20;
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AF528206.1 GI:32810973
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17; Conservative
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A new genotype of hereitis b virus
Patent: WO 0138498-A 31-MAY-2001;
Pharmasset, Inc. (US) : INNOGENETICS N.V. (BE)
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'specific host="Homo sapiens"
'db_xref="taxon:10407"
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/note="contains partial basal core promoter"
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                                                                                    linear
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/note="contains complete precore region"
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                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                    DNA
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100.0%; Score 20; DB
Best Local Similarity 85.0%; Pred. No. 16;
Matches 17; Conservative 3; Mismatches
                                                                                 AX151114 129 bp
Sequence 3 from Patent W00138498.
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 42 AGAGATGATTAGGCAGAGGT 23
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AF528205.1 GI:32810971
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AF528205/c
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Hepatitis B virus ASC1112 core antigen precursor, gene, partial
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Hepatitis B virus ASC20 core antigen precursor, gene, partial cds.
AF528207
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2 (bases 1 to 150)
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases I to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/specific_host="Homo sapiens"
/db_xref="taxon:10407"
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/note="contains partial basal core promoter"
                                                                                                          DB 14; Length 150;
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/translation="MQLFHLCLIISCSCPTVQASKLCLGWLXG"
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/codon_start=1
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/protein_id="AAP87557.1"
/db_xref="GI:32810974"
                                                                                                                                                            Indels
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                                                                                                  100.0%; Score 20; DB
85.0%; Pred. No. 15;
tive 3; Mismatches
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3; Mismatches
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/note="contains partial basal core promoter"
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AF528209/c
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                                                                                     Unpublished

2 (bases 1 to 150)

2 andhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Direct Submission

Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 150)
Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Gunission, Submission
Submitted (11-UUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
                   1 (bases 1 to 150)
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
                                                                                                                                                                                                                                                                                                             /isolation_source="asymptomatic HBsAg carrier"
/specific_host="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
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/specific_host="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="contains complete precore region"
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/protein_id="AAP87558.1"
/db_xref="GI:32810976"

    .150
    /organism="Hepatitis B virus"

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                                                                                                                                                                                                                                                           /proviral
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Best Local Similarity 85.0°
Matches 17; Conservative
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AF528209 150 bp DNA linear VRL 31-JUL-2003
Heparitis B virus ASC58 core antigen precursor, gene, partial cds.
AF528209
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(Unpublished
2 (bases 1 to 150)

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India

Location/Qualifiers
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Gandho'S.S., (Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
64. .>150
/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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AFF28210.
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/specific_host="Homo sapiens"
/db_xrefe<sup>#</sup>taxon:10407"
/country="India"
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/protein id="AAR87559.1"
/db_xref="GI:32810979"
/translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
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                                                                                                                         DB 14; Length 150
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'isolate="ASC58"
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Local 17; Conserve
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AF528212/c
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AF528213/c
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Hepatitis B virus

Hepatitis B virus

Hepatitis B virus

Hepatitis B virus

Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

I (bases 1 to 150)

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations

L Unpublished

E (bases 1 to 150)

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Direct Submission

L Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411001, Indian increase.
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Hepatitis B virus ASC335 core antigen precursor, gene, partial cds.
AF528211
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Gandha, M. S., Walimbe, A.M. and Arankalle, V.A.
Gandha, M. S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
(bnpublished)
(bnpublished)
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(candhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/specific_host="Homo sapiens"
/country="India"
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'specific host="Homo sapiens"
db_xref="taxon:10407"
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/note="contains partial basal core promoter"
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Best Local Similarity 85.0%; Pred. No. 15;
Matches 17; Conservative 3; Mismatches 0; Indels
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/note="contains partial basal core promoter"
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                                                                                                                                                                                                                                                                                             /organism="Hepatitis B virus"
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/mol_type="genomic DNA"
/isolate="ASC470"
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/isolate="ASC335"
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Hepatitis B virus ASC404 core antigen precursor, gene, partial cds.
AF528213
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Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A. Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/specific host="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
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                                                                                            translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
                                                                                                                                                                  Length 150;
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/note="contains partial basal core promoter"
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/db_xref="GI:32810982"
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/protein_id="AAP87561.1"
/db_xref="GI:32810984"
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/organism="Hepatitis B virus"
/proviral
                                                                                                                                                 100.0%; Score &v, 85.0%; Pred. No. 15; erive 3; Mismatches
                                                                                                                                                                  Score 20; DB
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85.0%; Pred. No. 15;
:ive 3; Mismatches
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/isolate="ASC343"
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codon_start=1
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Best Local Similarity 85.0°
Matches 17; Conservative
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Hepatitis B virus
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Hepatitis B virus ASC424 core antigen precursor, gene, partial cds.
AF528215
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Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S. S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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/specific_host="Homo saplens"
/db_xref="taxon:1040?"
/country="India"
<1. .>150
/note="contains partial basal core promoter"
(64. .>150
/note="contains complete precore region"
                                                                                /codon_start=1
/product="core antigen precursor"
/product="core antigen precursor"
/product="di=3810988"
/translation="MQLFHLCLIISCSCPTVQASKLCLGWLWD"
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/note="contains partial basal core promoter"
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85.0%; Pred. No. 15;
ive 3; Mismatches 0; Indels
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protein_id="AAP87564.1"
/db_xref="G1:32810990"
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85.0%; Pred. No. 15;
:ive 3; Mismatches
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/isolate="ASC424"
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2 (bases 1 to 150)
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Best Local Similarity 85.04
Matches 17; Conservative
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AF528216/c
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AF528215/c
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Hepatitis B virus ASC423 core antigen precursor, gene, partial cds.
AF528214
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Birect Submission, Hepatitis Division, National Institute of
Submitted (II-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Submitted (11-UJU-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
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Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases I to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
Unpublished
  Hepatitis B virus
Hepatitis B virus
Viruses; Ba virus
Viruses; Brorid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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/specific_host="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
                                                                                                                                                                                                                                                                                                                                                                                                   /isolation source="asymptomatic HBsAg carrier"
/specific host="Homo sapiens"
/db_xref="taxon:10407"
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/db_xref="GI:32810986"
/translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
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/isolate="ASC423"
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/isolate="ASC404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /country="India"
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Best Local Similarity 85.09
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AF528214/c
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AF528218/c
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                                                                                                                                                                                                            Unpublished
2 (bases 1 to 150)
2 (bases 1 to 150)
2 bases 1 to 150)
Direct Submission
Submitted (11-JUJ-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
                                                                                       Hepatitis B virus
Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (Dases 1 to 150)
Gandhe, S.S., Chadba, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutante in Indian patients with diverse clinical manifestations
Hepatitis B virus ASC1035 core antigen precursor, gene, partial
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Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations Unpublished
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                              /isolation_source="asymptomatic HBsAg carrier"
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/baref="taxon:10407"
/country="India"
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AF528216.1 GI:32810991
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Best Local Similarity 85.09
Matches 17; Conservative
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DEFINITION
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Gandho,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Gandho,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Submitted Submission, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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1 (Dases 1 to 150)
Gandhe, S. S., Chadha, M.S., Wallmbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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/specific_nost="Homo sapiens"
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/note="contains partial basal core promoter"
64. .>150
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/protein id="ApAR97566.1"
db xref="G1:32810995"
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larity 85.0%; Pred. No. 15;
Conservative 3; Mismatches 0; Indels
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Best Local Similarity 85.09
Matches 17; Conservative
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Hepatitis B virus
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AF528222 150 bp DNA linear VRL 31-JUL-2003
Hepatitis B virus ASC298 core antigen precursor, gene, partial cds.
AF528222
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Hepatitis B virus ASC1029 nonfunctional core antigen precursor,
gene, partial sequence.
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                                                                                                                                64. .>150
/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
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/db_xref="taxon:10407"
/country="India"
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          /isolation_source="asymptomatic HBsAg carrier"
/specific_host="Homo sapiens"
/baref="taxon:10407"
/country="India"
                                                                                           <1. .>150
/note="contains partial basal core promoter"
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/note="contains partial basal core promoter"
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100.0%; Score 20; DB
Best Local Similarity 85.0%; Pred. No. 15;
Matches 17; Conservative 3; Mismatches
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Best Local Similarity 85.0%; Pred. No. 15;
Matches 17; Conservative 3; Mismatches
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AF528221/c
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

E 1 (bases 1 to 150)
S Gandhe, S. S., Chadha, W. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
L Unpublished
Unpublished
C (bases 1 to 150)
S Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Direct Submission
L Submitted (11-JUL-2002) Hepatitis Division, National Institute of virology, 20-A, Dr Ambeddar Road, Pune, Maharashtra 411001, India
150 bp DNA linear VRL 31-JUL-2003
Gene, partial sequence.
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
Location/Qualifiers
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations Unpublished
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Hepatitis B virus ASC1027 nonfunctional core antigen precursor, AF528220
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/baref="taxon:10407"
/country="India"
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AF528225/c
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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2 (Dases 1 to 150)
2 and be, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411001, India
                                                                  1 > (bases I to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations Unpublished
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/specific_host="Homo sapiens"
/country="India"
/country="India"
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/specific_host="Homo sapiens"
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/protein_id="AAR97567.1"
/db_xref="G1:12811000"
/translation="MQLFHLCLIISCSCPTVQASKLCLGWLWG"
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    organism="Hepatitis B virus"

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/isolate="ASC298"
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/isolate="ASC263"
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Hepatitis B virus ASC1062 nonfunctional core antigen precursor,
gene, partial sequence.
AF528226.1 GI:32811004
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Gandho, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-UUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
                                                                  64. .>150
/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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AF528225.1 GI:32811003
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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'specific host="Homo sapiens"
'db_xref="taxon:10407"
/country="India"
<1. >150
/note="contains partial basal core promoter"
                                                                                                                                                                                        14; Length 150;
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/note="contains partial basal core promoter"
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3; Mismatches
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/isolate="ASC1036"
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AF528228/c
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2 (bases 1 to 150)
2 (bases 1 to 150)
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Submitted, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
                                                  (Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A. Comparative evaluation of HBV precore and basal core promoter mutante in Indian patients with diverse clinical manifestations Unpublished

2. (basea I to 150)

Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.

Direct Submission

Submitted (11.-0102) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 150)
Gandho,S.S., (Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Hepatitis B virus ASC1065 nonfunctional core antigen precursor,
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Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/specific_host="Homo sapiens"
/db_xref="taxon:10407"
/country="India"
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'note="contains partial basal core promoter"
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/note="contains partial basal core promoter"
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/db_xref="taxon:10407"
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/isolate="ASC1062"
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/isolate="ASC1065"
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AF528227
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Hepatitis B virus ASC1072 nonfunctional core antigen precursor, gene, partial sequence.
AF528228.1 GI:32811006
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Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases; Lo 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
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|specific host="Homo sapiens"
|db_xref="taxon:10407"
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85.0%; Pred. No. 15;
ive 3; Mismatches 0; Indels
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100.0%; Score 20; DB
Best Local Similarity 85.0%; Pred. No. 15;
Matches 17; Conservative 3; Mismatches
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/isolate="ASC1072"
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Best Local Similarity 85.0
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AF528232/c
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Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations Unpublished
2 (bases 1 to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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Hepatitis B virus
Viruses, Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases 1to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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/specific_hoste="Homo sapiens"
/baref="taxon:10407"
/country="India"
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/specific_host="Homo sapiens"
/baref="taxon:10407"
/country="India"
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/organism="Hepatitis B virus"
/proviral
/mol type="genomic DNA"
/isolate="ASC1074"
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3; Mismatches
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/isolate="ASC1091"
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Hepatitis B virus ASC265 nonfunctional core antigen precursor, gene, partial sequence.
AF528232.1 GI:32811010
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Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Direct Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus Hepathasizidae, Orthohepadhavirus. Viruses; Retroid viruses; Retroid viruses; Hepadhaviridae, Orthohepadhavirus. (bases 1 to 150) Gandhe, S.S., Chadha, M.S., Wallmbe, A.M. and Arankalle, V.A. Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
1 (bases I to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
Umpublished
2 (bases I to 150)
Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation".
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/specific_host="Homo sapiens"
/db_xref="taxon:10407"
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tive 3; Mismatches
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/mol_type="genomic DNA"
/isolate="ASC265"
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96 AGAGATGATTAGGCAGAGGT 77
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AF528235/c
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(bases 1 to 150)

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.

Direct Submission

Submitted (11-4)01-2002) Hepatitis Division, National Institute of Submitted, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
               Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
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Gandhe,S.S., Chadha,M.S., Walimbe,A.M. and Arankalle,V.A.
Comparative evaluation of HBV precore and basal core promoter
mutants in Indian patients with diverse clinical manifestations
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/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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/note="contains complete precore region; nonfunctional
core antigen precursor due to mutation"
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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/db_xref="taxon:10407"
/country="India"
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3; Mismatches
                                                                                                              /mol_type="genomic DNA"
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AF528235 15-JUL-2003
Hepatitis B virus ASC1275 core antigen precursor, gene, partial
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Hepatitis B virus ASC1274 nonfunctional core antigen precursor,
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2 (bases 1 to 150)
2 (bases 1 to 150)
Blact Submission
Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
                                                                                                                                                                                                                                                              Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A. Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Hepatitis B Virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S.S., (hadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations
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Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Gandhe, S. S., Chadla, M.S., Walimbe, A.M. and Arankalle, V.A. Direct Submission
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specific host="Homo sapiens"
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protein_id="AAP87568.1"
db_xref="G1:32811014"
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Submitted (11-JUL-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
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Gandhe, S.S., Chadha, M.S., Walimbe, A.M. and Arankalle, V.A.
Direct Submission
Birect Submission
Birect (11-JUL-2002) Hepatitis Division, National Institute of
Submitted (11-JUL-2002) Hepatitis Division, National Institute of
Virology, 20-A, Dr Ambedkar Road, Pune, Maharashtra 411001, India
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/note="contains complete precore region; nonfunctional core antigen precursor due to mutation"
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Hepatitis B virus
Viruses, Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 150)
Gandhe, S. S., Chadha, M. S., Walimbe, A. M. and Arankalle, V. A.
Comparative evaluation of HBV precore and basal core promoter mutants in Indian patients with diverse clinical manifestations Unpublished
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Hepatitis B virus ASC1090 core antigen precursor, gene, partial
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                                                                                             organism="Hepatitis B virus"

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    /organism="Hepatitis B virus".

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1 AGAGAUGAUUAGGCAGAGGT 20
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Aad7759 HBV Genot
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AAQ04799 AAH42375

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Aav82689 Fulminant
Aav82689 Fulminant
Aav82692 Fulminant
Aav82695 Fulminant
Aav82695 Fulminant
Aav82695 Fulminant
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Aav82696 Fulminant
Aav82706 Wild type
Aav82707 Sequence
Aan00003 Sequence
Aan10055 Suffire nu
Aax88924 Hepatitis
Aad14316 Hepatitis
Aad14316 Hepatitis
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Aad14316 Hepatitis
Aad14316 Hepatitis
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Aac23285 DNA Seque
Aaz23285 DNA Seque
Aaz23285 DNA Seque
Aaz23285 DNA Seque
Aaz23286 DNA Seque
Aaz3286 DNA Seque
Aaz3288 DNA Seque
Aax83023 Amplifier
Aam0699 Hepatitis
Aav83023 Hepatitis
Aav83023 Hepatitis
Aav83023 Hepatitis
Aam0699 Hepatitis
Aav83023 Hepatitis

AAD14317 AAQ88310

AAD09091 AAH77562 AAD14316

9

ABS66412

AAZ23286 ADM16809 AAQ45797 AAV07794 AAVB3023 AAQ66722

11,000,000

AAS16093

AAC88880 ABT08252 ADF09463 *tag= a note= "Internucleotide linkages are phosphorothioate"

. .10 *tag= b 'note= "2'-OMe RNA"

Location/Qualifiers

*tag=

/*tag= c
mod_base= OTHER
note= "2'-O-methyladenosine"

*tag= e mod_base= OTHER note= "2'-0-methyladenosine"

/*tag= d /mod_base= gm

/*tag= g
mod_base= OTHER
note= "2'-O-methyladenosine"

'mod_base= gm

*tag=

/*tag= h /mod_base= um

/*tag= i /mod_base= gm

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Hepatitis B virus RNA antisense oligonucleotide HBV43Ma.
                                                        HBV; HBV infection; inhibition; replication; ss.
                         03-SEP-1997 (first entry)
                                                                                      Key
misc_feature
                                                                                                                                           modified_base
                                                                                                                                                                         modified base
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                                                                                                                                                                                                                             modified base
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                                                                                                                                                                                                                                                                                                        modified base
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                                                                       Synthetic
           AAT72561;
                                                                                                                    misc_RNA
   Human hep
Human hep
Human hep
   hep
hep
hep
                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a synthetic oligonucleotide HBV43a which lat complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non- contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                                             /*tag= a
/note= "Internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                          Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
   Human
Human
Human
                                                                                                                                                                                                                                                                                                                      Mills JS
Aat73885 I
Aat05545 I
Aat73892 I
Aat73890 I
Aat73887 I
Aat73889 I
                                                                                                                                                                                                                                                                                                                      Kilkuskie RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 2; Length 20; 85.0%; Pred. No. 5.8; ative 3; Mismatches 0; Indels
                                                                                                                                                Hepatitis B virus RNA antisense oligonucleotide HBV43a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 7 A; 1 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                              HBV; HBV infection; inhibition; replication;
                                                                                                                                                                                                                                                                                                                      Jupp R,
                                                              ALIGNMENTS
        AAT05545
AAT73892
AAT73890
AAT73887
AAT73889
 AAT73885
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                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     Goodchild J,
                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 12; 81pp; English.
                                                                                                    BP.
                                                                                                                                                                                                                                                                 96WO-EP002432
                                                                                                                                                                                                                                                                                95US-00467397
                                                                                                    20
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                    Craig CJ, Frank BL, Good
Roberts NA, Roberts PC,
                                                                                                  AAT72560 standard; DNA;
 1. .20
/*tag=
                                                                                                                                                                                                                                                                                                                                           WPI; 1997-043124/04.
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Best Local Similarity
Local 17; Conserve
95.0
                                                                                                                                                                                            Key
misc_feature
                                                                                                                                                                                                                                                                04-JUN-1996;
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 100100
                                                                                                                                                                              Synthetic.
                                                                                                                  AAT72560;
                                                                                    RESULT 1
                                                                                            AAT72560
95
97
98
98
100
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Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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*tag= j
mod base= OTHER
note= "2'-O-methyladenosine"
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                                                                                                                                                                                                                                                                                  (HYBR-) HYBRIDON INC.
                                                                                                                                                                                                                                                                                                                                Craig CJ, Frank BL, Goodchild
Roberts NA, Roberts PC, Slade
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 12; 81pp; English.
                                                             /*tag= k
/mod_base= um
                                                                                                         /*tag= 1
/mod_base= um
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                                               modified base
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Gaps

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1 AGAGAUGAUUAGGCAGAGGT 20

AAT72561 ID 'AAT72561 standard; DNA; 20 BP.

RESULT 2

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llarity 85.0%; Pr Conservative 3;

20 22

1 AGAGAUGAUUAGGCAGAGGT AGAGAUGAUUAGGCAGAGGU

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Magnetic glass particle; nucleic acid purification; PCR primer; ss.

Reverse PCR primer used to amplify a HBV DNA fragment

(first entry)

22-AUG-2001 AAH25416;

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BP

AAH25416 standard; DNA; 27

RESULT 4 AAH25416/

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The present sequence represents a synthetic oligonucleotide HBV43Ma which
                            is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a single-stranded DNA probe (I) comprising in 3'-5' order, an anti-target nucleic acid segment, a (-)-promoter segment functionally linked to the anti-target segment, and a nucleic acid reporter segment. The probe is useful for testing a sample of a nucleic acid for the presence of a target nucleic acid segment or for detecting a target nucleic acid segment or also be used for the detection of hepatitis B virus (HBV). The probe nucleic acid segment contains the present about the detection of hepatitis B virus (HBV). The present sequence represents a bacteriophage SPG RNA polymerase promoter sequence sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single-stranded DNA probe comprising an anti-target nucleic acid, a (-)-promoter segment linked to the anti-target segment and a reporter segment, useful for detecting a target nucleic acid, e.g. hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from the present invention. (Updated on 15-
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                     100.0%; Score 20; DB 2; Length 20; 100.0%; Pred. No. 5.8;
                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis B virus; HBV; detection; probe; promoter;
                                                                                                                                                      Sequence 20 BP; 7 A; 1 C; 8 G; 1 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SP6 RNA polymerase promoter sequence SEQ ID NO:3.
                                                                                                                                                                                                100.0%; Preα. αν.
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Col 19-20; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schumm JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                           1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                   1 AGAGAUGAUUAGGCAGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                   AAA88131 standard; RNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                         Local Similarity 100.
1es 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteria phage SP6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-542420/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus, in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1991;
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13-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAA88131;
                                                                                                                                                                                      Query Match
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                                                                                                                                                                        /*tag= a
/note= "derivatisation with a p-(t-butyl)benzyl-residue"
                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of magnetic glass particles for purification of DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus RNA antisense oligonucleotide HBV88b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 BP; 5 A; 10 C; 2 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 20; DE
Best Local Similarity 85.0%; Pred. No. 6;
Matches 17; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purified using the method of the invention
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Page 99; 105pp; English
                                                                                                                                                                                                                                                                                                                                                             Geiger A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGAGAUGAUUAGGCAGAGGT 20
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                                                                                                                                                                                                                                                                                                        12-MAY-2000; 2000EP-00110165
                                                                                                                                                                                                                                                                                                                                                                                                                              RNA in automated processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT72562 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-381247/40.
                                                                                                                   Hepatitis B virus.
                                                                                                                                                                                                              WO200137291-A1
                                                                                                                                            Key
modified_base
                                                                                                                                                                                                                                                                                          17-NOV-1999;
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Gaps ö

0; Indels

Score 20; DB 3; Length 25; red. No. 5.9;

Query Match
100.0%; Score 20; DE
Best Local Similarity 95.0%; Pred. No. 5.9;
Matches 19; Conservative 1; Mismatches

Sequence 25 BP; 10 A; 1 C; 10 G; 0 T; 4 U; 0 Other;

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96WO-EP002432
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*tag=
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                                                                                                    Frank BL,
                                                                                                                                              WPI; 1997-043124/04.
04-JUN-1996;
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                           06-JUN-1995;
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                                                                                                 Craig CJ, F
Roberts NA,
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Matches
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                                                                                                /*tag= a
/note= "Internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                             Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "Internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                          Mills JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus RNA antisense oligonucleotide HBV-87b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 12 A; 3 C; 10 G; 5 T; 0 U; 0 Other;
    HBV; HBV infection; inhibition; replication; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HBV; HBV infection; inhibition; replication; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                          Jupp
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                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                       Goodchild J,
PC, Slade A;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 12; 81pp; English.
                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO (HYBR-) HYBRIDON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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es 17; Conservative
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                                                                                                                                                                                                                                                                                                    Craig CJ, Frank BL, Goor
Roberts NA, Roberts PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                misc_feature
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misc_feature
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                                   Synthetic
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Matches

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                                                                                                                                                 Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
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"Internucleotide linkages are phosphorothioate"
                                                                           Mills JS;
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                           Kilkuskie RE,
                                                                                                                                                                                                                                                                                                                                                                             Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis B virus RNA antisense oligonucleotide HBV88Mb.
                                                                                                                                                                                                                                                                                                                                             Sequence 30 BP; 10 A; 2 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          / Match 100.0%; Score 20; DB 2; Local Similarity 85.0%; Pred. No. 6; nes 17; Conservative 3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HBV; HBV infection; inhibition; replication;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= f
/mod_base= OTHER
/note= "2'-0-methyladenosine"
                                                                           Jupp R,
                            [다
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                          (HOFF ) HOFFMANN LA ROCHE & CO AG (HYBR-) HYBRIDON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGAGAUGAUUAGGCAGAGGT 20
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                                                                        rank BL, Goodchild
Roberts PC, Slade
                                                                                                                                                                                            Claim 5; Page 15; 81pp; English.
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/note= "2'-OMe
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95US-00467397
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/mod_base=
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/mod base=
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Claim 1; Page 12; 81pp; English.

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Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mills JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jupp R, Kilkuskie RE,
                                                                                                                                                                                                                                                               mod_base= OTHER
note= "2'-0-methyladenosine"
                                                                                                                                                                                                                                                                                                                      *tag= q
mod_base= OTHER
note= "2'-O-methyladenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "2'-0-methyladenosine"
                                                                                                                                               *tag= 1
mod_base= OTHER
note= "2'-0-methyladenosine"
                                                              note= "2'-0-methyladenosine'
                                                                                 '*tag= j
mod_base= OTHER
'note= "2'-O-methyladenosine'
                                                                                                                                                                                      *tag= m
mod_base= OTHER
note= "2'-O-methyladenosine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craig CJ, Frank BL, Goodchild J,
Roberts NA, Roberts PC, Slade A;
                                           g= i
_base= OTHER
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nod base= OTHER
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mod_base= cm
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mod_base= gm
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mod_base= gm
mod base= um
                /*tag= h
/mod_base= gm
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mod_base= gm
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/mod_base= um
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mod ba
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                  The present sequence represents a synthetic oligonucleotide HBV88Mb which is complementary to a portion of the hepatitis B virus (HBV) RNA. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides containing a sequence which is complementary to at least two non-contiguous regions of an HBV nucleic acid, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
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*tag= a
note= "Internucleotide linkages are phosphorothioate"
                                                                                                                                                              Gaps
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                                                                                                                                    Query Match
100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus RNA antisense oligonucleotide HBV-87Mb
                                                                                                              Sequence 30 BP; 12 A; 3 C; 10 G; 1 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                  HBV, HBV infection; inhibition; replication; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/mod_base= OTHER
/note= "2'-0-methyladenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= e
/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-0-methyladenosine"
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/mod_base= OTHER
/note= "2'-O-methyladenosine"
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            l. .10
/*tag= b
'note= "2'-OMe RNA"
                                                                                                                                                                                    1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                 11 AGAGAUGAUUAGGCAGAGGT 30
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/mod_base= gm
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/mod_base= um
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/mod_base= um
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/mod_base= gm
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The present invention describes a method of screening for an antiviral agent by the protein-priming activity of hepatitis B virus (HBV) DNA polymerase. Also described is developing an antiviral agent with a high selectivity to HBV which can be used for high-throughput screening. The present sequence represents an RNA oligonucleotide which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single-stranded DNA probe comprising an anti-target nucleic acid, a (-)-promoter segment linked to the anti-target segment and a reporter segment, useful for detecting a target nucleic acid, e.g. hepatitis B
                       Screening of antiviral agents by protein-priming activity of hepatitis virus DNA polymerase.
                                                                                                                                                                                                                                                           100.0%; Score 20; DB 10; Length 39; 85.0%; Pred. No. 6.2; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus; HBV; detection; probe; promoter; ds.
                                                                                                                                                                                                                           Sequence 39 BP; 5 A; 13 C; 3 G; 0 T; 18 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SP6 RNA polymerase promoter sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Col 19-20; 18pp; English.
                                                                      Disclosure; Page 12; 13pp; Korean.
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                                                                                                                                                                                                                                                                                                                                                27 AGAGATGATTAGGCAGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteria phage SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROM-) PROMEGA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-542420/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus, in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-1991;
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AAA88130/
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                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a synthetic oligonucleotide HBV-87Mb which contains a sequence which is complementary to at least two noncontiguous regions of a hepatitis B virus (HBV) nucleic acid. The antisense oligonucleotide may be used to detect the presence of HBV in a sample. The antisense oligonucleotide, and oligonucleotides complementary to a portion of the HBV RMA, may be used for inhibiting HBV replication in a cell or for the treatment of HBV infection
                                                                                                                                                                                                                                                                                                                                    Oligo:nucleotide(s) complementary to hepatitis B virus (HBV) sequences used in the detection and treatment of HBV infection.
                                                                                                                                                                                                                                                         Mills JS;
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                                                                                                                                                                                                                                                        Kilkuskie RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 2; Length 30; 100.0%; Pred. No. 6; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 BP; 10 A; 2 C; 12 G; 3 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                         Jupp R,
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                                                                                                                                                                                                                                                      Goodchild J,
PC, Slade A;
                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE & CO AG (HYBR-) HYBRIDON INC.
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                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 15; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGAGAUGAUUAGGCAGAGGT
                               /mod_base= um
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                   *tag= 1
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                                                                                                                                                                                                                                                                      Roberts PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                      Frank BL,
                                                                                                                                                                                                                                                                                                      WPI; 1997-043124/04.
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Best Local Similarity
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modified base
                                                                 WO9639502-A1
                                                                                                                                   04-JUN-1996;
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Roberts NA,
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Best Loca Matches

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The present invention describes a single-stranded DNA probe (1) comprising in 3.-5 order, an anti-target nucleic acid segment, a (-)-promoter segment functionally linked to the anti-target segment, and a nucleic acid reporter segment. The probe is useful for testing a sample of a nucleic acid for the presence of a target nucleic acid segment or for detecting a target nucleic acid segment or also be used for the detection of hepatitis b virus (HBV). The probe may agenence represents a bacteriophage SPG RNA polymerase promoter sequence which is used in an example from the present invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64 BP; 14 A; 22 C; 4 G; 24 T; 0 U; 0 Other;
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33 AGAGATGATTAGGCAGAGGT 14

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Gарв

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AAD09093 standard; DNA; 129

AAD09093/c

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The present invention relates to hepatitis B virus (HBV) strain FR1, genotype G DNA encoding PreCore/Core protein, HBpol, envelope (PreS1, PreS2 and surface antigen HBBAg) and HBX proteins. HBP genotype G nucleic acids and surface artispen HBAg) and HBX proteins. HBV genotype G nucleic acids and polypeptides are useful for diagnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to incleic acids and antibodies are useful for detecting HBV genotype G in a sample or diagnosis of HBV genotype G infection. The presence of HBV genotype G statistically correlates with the presence of liver damage cand/or liver cancer in the subject. The HBV genotype G core insert peptide encoding nucleic acid is useful for designing monitoring assays to study and predict the evolution of anti-HBe and anti-HBc antibodies and HBAG (genotype G e antigen) in patients infected with HBV. The antibodies or antigens of HBV genotype G are useful for identifying a stage of liver disease caused by HBV genotype G. The present sequence is a hepatitis B virus (HBV) strain FRI, genotype G DNA fragment encoding e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
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                                                                                                                                                                                                                                                                                                                                                                     HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; HBeAg; liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.
                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus FR1 strain genotype G HBeAg DNA fragment.
100.0%; Score 20; DB 3; Length 64;
                                      Indels
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                  85.0%; Pred. No. 6.6;
:ive 3; Mismatches
                                                                           1 AGAGAUGAUUAGGCAGAGGT 20
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                                                                                                  23 AGAGATGATTAGGCAGAGGT 4
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                  Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-367676/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
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  Query Match
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genotype G DNA encoding Precore/Core protein, HBpol, envelope (Presi, Press and surface antigen HBaAg) and HBX proteins. HBvG envelope (Presi, Press and surface antigen HBaAg) and HBX proteins. HBV genotype G muclatic acids and polypeptides are useful for disgnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to treat or prevent HBV genotype G infection. The HBV genotype G derived mucleic acids and antibodies are useful for detecting HBV genotype G in a sample or disgnosis of HBV genotype G infection. The presence of HBV genotype G statistically correlates with the presence of liver damage and/or liver cancer in the subject. The HBV genotype G core insert peptide encoding nucleic acid is useful for designing monitoring assays to study. A predict the evolution of anti-HBC and anti-HBC antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and HBeÂg (genotype G e antigen) in patients infected with HBV. The artibodies or antigens of HBV genotype G are useful for identifying a stage of liver disease caused by HBV genotype G. The present sequence is a hepatitis B virus (HBV) strain FRI, genotype G DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zoulim F, Fried M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                       HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease; hepatitis; liver cancer; HBcAg; core antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to hepatitis B virus (HBV) strain FR1
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                                                                                                                  Hepatitis B virus FR1 strain genotype G DNA fragment #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Geyt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB
85.0%; Pred. No. 7.1;
iive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               99US-0167206P.
                                                                                                                                                                                                                                                                                                                                                    21-NOV-2000; 2000WO-US032108.
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nes 17; Conservative
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stuyver L, Schinazi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAR-) PHARMASSET INC. (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-367676/38.
                                                                                                                                                                                                                                     Hepatitis B virus.
                                                                                                                                                                                                                                                                            WO200138498-A2
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                                                                           04-SEP-2001
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                                      AAD09093;
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Gaps

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100.0%; Score 20; DB 4; Length 87; 85.0%; Pred. No. 6.8; cive 3; Mismatches 0; Indels

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1 AGAGAUGAUUAGGCAGAGGT 20

Local Similarity 85.0 nes 17; Conservative

Query Match Matches ...

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(first entry)

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Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
vand promoter; androgen receptor promoter; Apromoter;
human epidermal growth factor receptor 2 promoter; her2 promoter;
beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer
colon cancer; immunological disorder; prostate cancer; cytostatic;
autoimmune disease; HBV promoter; HBV-X promoter;
Enterococcus infection; immunosuppressive; antibacterial; antiviral;
gene expression modulator; multiple sclerosis; MS;
chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
                                       Wild type hepatitis B virus core promoter.
                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-2001; 2001WO-US018343
                                                                                                                                                                                                     Hepatitis B virus.
                                                                                                                                                                                   transgenic; ds.
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                     23-APR-2002
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 ABK29867
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Location/Qualifiers

/bound_moiety= "HNF3-1" /note=="Hepatocyte nuclear factor 3-1" 115. .126 /*tag= c /bound_moiety= "HNF3-2" /note= "Hepatocyte nuclear factor 3-2" /bound_moiety= "HNF4" /note=""Hepatocyte nuclear factor 4" tag= /*tag=

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06-JUN-2000; 2000US-0209549P.

(GENE-) GENELABS TECHNOLOGIES INC.

AW, Laurance ME, Michelotti EF; , Thomas RL, Kongpachith A, Sheppard LT; Latour DR, Starr DB, Tam Velligan MD, Latou Lim MY, Bruice TW; Kim JP,

WPI; 2002-130595/17.

New nucleic acid regulatory sequences, which are able to regulate expression of a gene operably linked to a promoter, useful for regulating the expression of transgenes and for treating e.g., cancer and immunological diseases.

Disclosure; Fig 1A; 95pp; English.

The invention describes an isolated nucleic acid regulatory sequence for a cyclin D1 promoter, a CD4OL promoter, vancomycin-resistant enterococci (VRE) promoter, an HBV promoter, androgen receptor (RA) promoter, Human epidermal growth factor receptor 2 (HBR2) promoter, or a beta lattamase (Bla) promoter. Transcription regulatory sequences may be used to requlate expression of the endogenous, autologous or heterologous genes operably linked to the promoter, and may be incorporated into heterologous nucleic acid constructs for use in regulated expression of transgenes. Regulated expression of cyclin D1 can be used in cancer therapies, such as breast, colon or pancreatic cancers and familial adenomatous polyposis. Regulation of the activity of CD4OL gene promoter may be used in the treatment of immunological disorders, such as autoimmune diseases e.g. multiple sclerosis (MS), systematic luques erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid

arthritis. Regulated expression of genes under the control of the HBV (hepatitis B)-specific core, pre-5 and X promoters can be used in the therapy of HBV disease, chronic hepatic insufficiency, cirrhosis, hepatocellular carcinoma, and in the regulated expression of liver specific genes. Regulated expression of the vanH gene promoter can be used in treatment of Enterococcus infection, while regulated expression of the androgen receptor gene can be used in the treatment of prostate cancer. This sequence represents the hepatitis B virus core promoter the regulatory regions of which are described in the method of the invention 888888888888888

Sequence 250 BP; 66 A; 59 C; 62 G; 63 T; 0 U; 0 Other;

Gaps ö Length 250; 0; Indels ; Score 20; DB 6; Pred. No. 7.6; 3; Mismatches 0; 100.0%; 85.0%; P Query Match
Best Local Similarity 85.0
Matches 17; Conservative

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248 AGAGATGATTAGGCAGAGGT 229 20 1 AGAGAUGAUUAGGCAGAGGT 셤 ò

AAD27422,

AAD27422 standard; DNA; 639

AAD27422;

(first entry) 18-APR-2002 Hepatitis B virus (HBV) core antigen (HBcAg) encoding DNA #1.

Hepatitis B virus; HBV; core antigen; HBCAg; immune system; typhoid; prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes; hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea; tuberculosis; polio; rabies; acquirred immunodeficiency syndrome; AlDS; dengue fever; yellow fever; malaria; whooping cough; salmonellosis; antiprotozoal; servingitis; gonorrhea; antiviral; antibacterial;

Hepatitis B virus.

Location/Qualifiers /product= "HBcAg" ď .639

WO200198333-A2,

27-DEC-2001.

22-JUN-2001; 2001WO-GB002817.

22-JUN-2000; 2000GB-00015308. 06-OCT-2000; 2000GB-00024544.

(CELL-) CELLTECH PHARM LTD.

Li J, Pumpens P; Page M,

WPI; 2002-098223/13. P-PSDB; AAE17018. New proteins comprising a modified hepatitis B core antigen, useful as a vaccine in prophylactic or therapeutic vaccination of the human or animal body, particularly against hepatitis B virus infection.

Disclosure, Page 38-39; 40pp; English.

The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBCAg) wherein one or more of the four arginine repeats has been deleted and the protein comprising the C-terminal cysteine of HBCAg. The deleted region may be replaced by an epitope from a protein other than HBCAg, in which case the HBCAG acts as a carrier to

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Gaps ö

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therapeutic vaccination of the human or animal body, particularly against therapeutic vaccination of the human or animal body, particularly against HBV. The nucleic acid encoding the protein may be used in gene therapy or DNA vaccination protocols. The chimeric protein or its nucleic acid may also be used as the basis of a prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth disease, polio, herpes, rabies, acquired immunodeficiency syndrome (AIDS), dengue fever, yellow fever, malaria, diarrhoea, meningitis or gonorrhea. The present sequence is a DNA encoding Hepatitis B virus core antigen (HBCAG)
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prophylactic or therapeutic treatment of humans or animals against e.g.
HB virus, viral hepatitis, hepatitis C virus, influenza, or foot-and-
   present the epitope to the immune system. This chimeric protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus core antigen; HBcAg; prophylactic; viral hepatitis; therapeutic; vaccine; acquired immune deficiency syndrome; influenza; polio; herpes; rabies; AIDS; foot-and-mouth disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 20; DB 6; Length 639;
Pred. No. 8.4;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
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/*tag= a
/product= "HBc protein"
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P-PSDB; AAE19793.
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ID AAD31509/C
AC AAD3150
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AC AAD3150
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The present invention relates to hepatitis B virus (HBV) core antigen

Disclosure; Page 23-24; 27pp; English

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(HBCAg) fusion proteins and polynucleotides encoding such proteins. Sequences of the invention are useful in methods of prophylactic or therapeutic vaccination or to manufacture medicaments for prophylactic or therapeutic vaccination of the human or animal body sgainst HBV, e.g. against viral hepatitis. They are also useful as a prophylactic vaccine against e.g. hepatitis c virus, influenza, polio, herpes, rables, acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The
                                                                                       acquired immune deficiency syndrome (AIDS) or foot-and-mouth disease. The present sequence is a DNA encoding hepatitis B virus core antigen (HBCAg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of introducing nucleic acid molecules to an animal which comprises administering a composition comprising two or more gene delivery vehicles to an animal at the same time and same site via a single administration device. The method is useful for introducing nucleic acid molecules to an animal, preferably humans for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Introducing nucleic acid molecules to an animal or human, useful for treating diseases including cancer, genetic diseases, arthritis or AIDS comprises administering a composition comprising two or more gene delivery vehicles.
                                                                                                                                                                                             Gaps
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                                                                                                                                                                Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ds; precore/core; cancer; genetic disease; arthritis; AIDS.
                                                                                                                                  Sequence 639 BP; 147 A; 161 C; 141 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                            0; Indels
                                                                                                                                                                DB 6;
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                                                                                                                                                             100.0%; Score 20; DB
85.0%; Pred. No. 8.4;
ive 3; Mismatches
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9005-0056566
9005-0056663
9105-00830417
9205-0095084
9305-00102132
9305-00102132
9305-0010424
9305-00105394
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                                                                                                                                                                                                                                                                                                                              ADL56756 standard; DNA; 646
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                                                                                                                                                                                            17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    HBV precore/core DNA.
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(MONT/) MONTISANO D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-282522/26.
                                                                                                                                                                            Similarity
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treating diseases including cancer, genetic diseases, arthritis or AIDS. The method can also be administered to plants using traditional methods. The introduction of multiple or more than one nucleic acid molecule at one time provide significant advantages because multiple nucleic acid molecules can provide complementary substances or activities to a single nucleic acid molecules is much less than engineering a single nucleic acid molecules is much less than engineering a single molecule is multiple molecules, there is less chance that one substance or activity will sterically hinder or otherwise interfere with another substance or activity. The use of multiple molecules also permits systems subject to different substances or activities from expression control of different activity activity used of activity activities from expression control of different substances or activities. The present sequence represents the HBV precore/core DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Precore; core; coding region; hepatitis B; virus; HBV; plasmid; KSII+; KSII+HBpc/c; pAMG; deletion; frameshift; PCR; overlap extension; SK+ HBe; primers; mutation; hepatocellular carcinomas; class-I; cytotoxic T-lymphocyte; CTL; hepatitis C; infection; ss.
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/note= "Nucleotide which is deleted in plasmid pAM6"
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                                                                                                                                                                                                                                                                                      Sequence 646 BP; 154 A; 170 C; 137 G; 185 T; 0 U; 0 Other;
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(revised)
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Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-258682/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
31-JAN-1994
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Gaps

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containing the entire precore/core region, into the BamHI site of KSII+. The precore/core region of plasmid KSII+HBpc/p was sequenced and was found to contain a single base pair deletion which causes a frameshift at codon 79 which results in two consecutive in-frame TAG codons. This deletion was corrected by PCR overlap extension in plasmid SK+ HBe using mutation may also be corrected using the primers given in AAQ47015-18 in four separate reactions. The a separate series of reactions. The isolated HBV precore/core region may be used in a method to induce potent class-I restricted protective and therapeutic cytoxic T-lymphocyte (TLI) response, and a humoral response for the treatment of hepatitis B and C infections, as well as hepatocellular carcinomas. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Precore; core region; HBV; hepatitis B virus; gene delivery vehicle; GDV; immunogen; HBV antigen; hepatitis C cardinoma cell; HBV infection; gene expression; non-tumourigenic tumour associated antigen; therapy; altered ras gene; altered psi gene; altered mucin; ss.
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(HBV) genome. This sequence can be included in a gene delivery vehicle
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Introduction of nucleic acid molecules to an animal - comprises administration of two or more gene delivery vehicles comprising heterologous nucleic acid.
                                                                                                                                                                                                                                                                Length 655;
                                                                                                                                                                                                                             Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                           100.0%; Score 20; DB 2;
85.0%; Pred. No. 8.5;
iive 3; Mismatches 0;
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/*tag= a
/note= "precore region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Precore/core region of HBV.
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25-FEB-1997
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This sequence represents the entire precore/core coding region of hepatitis B virus (HBV) isolated from the plasmid KSII+HBpc/c. This plasmid was created by ligating a 1.8 kb fragment of plasmid pAM6

Example 2; Fig 2; 110pp; English.

antigen.

introducing nucleic acids into an animal, by administration of a composition comprising two or more GDVs, in combination with a carrier or contained comprising two or more GDVs, in combination with a carrier or contained within the GDV, or directs expression of at least one substance (or biologically active nucleic acid) in host cells containing the GDV. The two GDVs collectively direct the expression of at least two different substances, or direct the expression of at least two different GDVs differ in one or more biological functions. The GDVs can be used for destroying hepatitis C carcinoma cells, for treating HBV (when a GDV contains an immunogenic HBV fragment such as this sequence). The GDVs can also be used for directing expression of non-tumourigenic, tumour associated antigens (such as altered ras gene), altered p53 gene, and (GDV) of the invention, and is used as an immunogenic portion of a HBV altered mucin. (Updated on 27-AUG-2003 to correct OS field.) \$

Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;

100.0%; Score 20; DB 2; Length 655; 0; Indels 85.0%; Pred. No. 8.5; ive 3; Mismatches 1 AGAGAUGAUUAGGCAGAGGT 20 43 AGAGATGATTAGGCAGAGGT 24 Best Local Similarity 85.0 Matches 17; Conservative Query Match ઠે 셤

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Gaps

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AAH77569 standard; DNA; 655 BP. RESULT 19

19-OCT-2001 (first entry) AAH77569;

HBV genotype G strain US1 preCore/Core DNA.

Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPol; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg; HBeAg; ds.

Hepatitis B virus.

WO200140279-A2.

07-JUN-2001

20-NOV-2000; 2000WO-EP011526.

99EP-00870252 99US-0169287P 03-DEC-1999; 07-DEC-1999;

WPI; 2001-374785/39.

(INNO-) INNOGENETICS NV

Stuyver L, Van Geyt C,

De Gendt S;

WPI; 2001-374785/39

HBV Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy

Claim 3; Fig 7; 94pp; English.

The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in sepecification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by AAH77569/
ID AAH77569/
XX AAC AAH77
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XX XX Hepal

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ö eample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting the proteins and for detecting the proteins and the detecting preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/fore sequences of an HBV genotype A strain (HBVKCPS) and 7 strains (FR1, FR2, US1, US3, US3, US3, US1) of HBV genotype G polynucleotides are useful for detecting antibodies in a biological Gaps Hepatitis B virus, HBV, preCore, Core, preSl, preS2, HBS, HBK, HBsAg; antiviral, vaccine, genotype G; genotype A; genotyping; HBeAg; ds. ö DB 4; Length 655; 8.5; Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other; 0; Indels Pred. No. 8.5; 3; Mismatches HBV genotype G strain FR2 preCore/Core DNA. 100.0%; Score 20; ŝ De Gendt 1 AGAGAUGAUUAGGCAGAGGT 20 33 AGAGATGATTAGGCAGAGGT 14 20-NOV-2000; 2000WO-EP011526. 03-DEC-1999; 99EP-00870252. 99US-0169287P 82.0%; AAH77568 standard; DNA; 655 19-OCT-2001 (first entry) Query Match Best Local Similarity 85.0° Matches 17; Conservative Stuyver L, Van Geyt C, (INNO-) INNOGENETICS NV. Hepatitis B virus. WO200140279-A2. 07-DEC-1999; 07-JUN-2001. AAH77568; AAH77568/c RESULT 20 8888888888888 ઠે g

The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the UGA. The invention relates to a fully defined sequence of 3248 nucleotides as given in sequence, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins antibodies directed against the proteins are useful for detecting the proteins and for detecting the proteins and sequence in medicament for treating HBV infections. The preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRZ, USI, US3, Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and Claim 3; Fig 7; 94pp; English.

HBPol; HBCAg;

Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBeAg; ds.

Hepatitis B virus.

WO200140279-A2.

07-JUN-2001.

20-NOV-2000; 2000WO-EP011526.

99EP-00870252.

03-DEC-1999; 07-DEC-1999;

(INNO-) INNOGENETICS NV

HBV genotype G strain US7 preCore/Core DNA.

(first entry)

19-0CT-2001

AAH77573;

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AAH77573 standard; DNA; 655

AAH77573/c ID AAH77

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Gaps

1 AGAGAUGAUUAGGCAGAGGT 33 AGAGATGATTAGGCAGAGGT

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Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                           Hepatitis B virus, HBV, preCore, Core, preSl, preS2, HBS, HBX, HBPOl, HBAAG, antiviral, vaccine, genotype G, genotype A, genotyping, HBcAG;
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                                  Query Match
100.0%; Score 20; DB 4; Length 655;
Best Local Similarity 85.0%; Pred. No. 8.5;
Matches 17; Conservative 3; Mismatches 0; Indels
                 Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;
                                                                                                                                                                                         HBV genotype G strain US10 preCore/Core DNA.
US6, US7, US9, US10) of HBV genotype G
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07-DEC-1999; 99US-0169287P.
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The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention sequence that is degenerate to the mentioned sequence. These specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polymucleotides are useful for HBV genotyping. The proteins encoded by the polymucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and for detecting the proteins are useful for detecting the proteins and sainst the proteins are useful for detecting the proteins and sainst the proteins are useful for detecting the proteins and so useful for preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/CC an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRI, US3, US1, US3, US1) of HBV genotype G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig 7; 94pp; English.
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RESULT 23

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Query Match
100.0%; Score 20; DB 4; Length 655;
Best Local Similarity 85.0%; Pred. No. 8.5;
Matches 17; Conservative 3; Mismatches 0; Indels

Sequence 655 BP; 144 A; 156 C; 143 G; 206 T; 0 U; 6 Other;

Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBeAg; ds.

Hepatitis B virus.

WO200140279-A2

07-JUN-2001

HBV genotype G strain USS preCore/Core DNA

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                                                                                                                                                                                                                  Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS; HBX; HBPO1;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
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                              AAH77570 standard; DNA; 655 BP
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Best Local Similarity 85.0°
Matches 17; Conservative
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Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and

Claim 3; Fig 7; 94pp; English.

De Gendt S;

Stuyver L, Van Geyt C, (INNO-) INNOGENETICS NV

WPI; 2001-374785/39.

20-NOV-2000; 2000WO-EP011526. 03-DEC-1999; 99EP-00870252. 07-DEC-1999; 99US-0169287P.

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The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and spreading the mediane the receive proteins for treating the sequence is provided in an alignment of precence/Core sequences of the W genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3, US6, US7, US9, US10) of HBV genotype G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis B; hepatitis C; immunogen; HBV; HCV; hepatocellular carcinoma; HCC; gene therapy; virucide; hepatotropic; antiinflammatory; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 AGAGATGATTAGGCAGAGGT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD21244 standard; DNA; 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD21244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
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Gaps ö

0; Indels

3; Mismatches

1 AGAGAUGAUUAGGCAGAGGT 20

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33

RESULT 24
AAH77571/C
ID AAH77571 standard; DNA; 655 BP.
XX
AC AAH77571;
XX
XX
DT 19-OCT-2001 (first entry)

Pred. No.

82.08;

rhinovirus; pox virus; canary pox virus; vaccinia virus; influenza virus; adenovirus parvovirus; adeno-associated virus; herpes virus; measles; corona virus; HIV; human immunodeficiency virus; Sindbis virus; virucide; hepatotropic; ds; precore/core DNA.

```
New vectors that direct the (co-)expression of one or more immunogenic portions of the hepatitis B or C virus antigen(s), useful in gene therapy, e.g. for treating or preventing hepatitis B or C infections, or hepatocellular cardinomas.
                                                                                                                                                                                                                      O'dea J;
                                                                                                                                                                                                                      Townsend K,
                                               /*tag= b
/note= "Core region"
replace(332. .334, CC)
/*tag= c
replace(338. .340, CAA)
/*tag= d
                        *tag= a
note= "Precore region'
         Location/Qualifiers
                                                                                                                                                                                                                                                                                           Example 2; Fig. 2; 64pp; English.
                                                                                                                                                                                                                      Lee WTL,
                                                                                                                                                     92US-00830417.
93US-00032385.
93US-00102132.
94US-00286829.
95US-00374414.
                                                                                                                                        95US-00483511
                                        .655
                                                                                                                                                                                                                     Jolly DJ, Chang SMW,
                                                                                                                                                                                                     (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                     WPI; 2001-647290/74.
              misc_feature
                                       misc_feature
                                                                                                       US6297048-B1
                                                                                                                                       07-JUN-1995;
                                                                                                                                                               17-MAR-1993;
                                                                                                                                                                      04-AUG-1993;
                                                                                                                      02-OCT-2001
                                                                                                                                                                                     19-JAN-1995;
                                                                                                                                                                              35-AUG-1994
                                                               mutation
                                                                                mutation
```

0'dea

Townsend K,

Lee WTL,

Chang SMW,

Jolly DJ,

SXXCCCCCCCCCCCCCCCXXXXXIXXBAPAPXXBXBBXXBXXBXXBXXBXXBXXBXXBXXBXXBXXBX

(ODEA/)

JOLLY D J.
CHANG S M W.
LEE W T L.
TOWNSEND K.
O'DEA J.

(JOLL/) (CHAN/) (LEEW/)

92US-00830417. 93US-00032385. 93US-00102132. 94US-00286829. 95US-00374414.

24-JUL-2001; 2001US-00912679,

04-FEB-1992; 04-AUG-1993; 05-AUG-1994; 07-JUN-1995;

Hepatitis B virus.

US2002141974-A1.

03-OCT-2002

The present invention relates to a method for treating hepatitis B or C directions. The method involves administering a vector construct that directs the expression of at least one immunoganic portion of hepatitis B virus (HBV) antigen, containing HBeAg, HbcAg, HbcAg, S. Pre-S1, Pre-S2, open reading frame (ORF) 5, ORF 6, HBV pol or HBxAg or co-expression of a least one immunogenic portion of a HBV antigen and at least one immunogenic portion of a hepatitis C virus (HCV) antigen. The vectors are useful in gene therapy, particularly for treating or preventing hepatitis The present sequence is a PCR primer used for amplifying Hepatitis B virus adw strain precore/core mutant DNA.

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Gaps
                                                                                              ö
                                             100.0%; Score 20; DB 4; Length 655; 85.0%; Pred. No. 8.5; ive 3; Mismatches 0; Indels
Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;
                                                                  Best Local Similarity 85.0
Matches 17; Conservative
```

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1 AGAGAUGAUUAGGCAGAGGT 20 43 AGAGATGATTAGGCAGAGGT 24 à 셤

RESULT 26
ABX80077/c
ID ABX80077 standard; DNA; 655 BP.
XX
AC ABX80077;
XX
DT 22-APR-2003 (first entry)
XX
XX
XX
XX
XX
WHEPATITIS B virus; hepatitis C vi:
XW Hepatitis B infection; hepatitis of the control of the con

Hepatitis B virus precore/core DNA.

Hepatitis B virus, hepatitis C virus, hepatitis C infection, poliovirus, hepatitis B infection, hepatitis C antigen; polyprotein antigen; SV40,

Hepatitis B virus (HBV) DNA.

(first entry)

15-MAY-2003

BXBXBXB

g ઠે

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The invention relates to a method for treating hepatitis C infections in a warm-blooded animal comprising administering a vector construct which directs the expression of at least one immunogenic portion of a hepatitis c antigen, where an immune response is generated, and alternatively, in combination with an immunodulatory cofactor. The invention also relates to a vector construct which directs the co-expression of at least one immunogenic portion of a hepatitis B antigen and at least one immunogenic portion of a hepatitis C antigen, an immunogenic portion of the polyprotein antigen, or an immunogenic portion of the polyprotein antigen and an immunoregulatory cofactor. A recombinant virus carrying the vector construct is selected from poliovirus, rhinovirus, pox virus, canary pox virus, vaccinia virus, influenza virus, adenovirus, parvovirus, adenovirus, herpes virus, SV40, HIV, measles, corona virus or singles virus. This sequence represents hepatitis B virus precore/core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                         Treating hepatitis C infections in a warm-blooded animal by administering a vector construct, which directs the expression of an immunogenic portion of a hepatitis C antigen, and alternatively, with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 9; Length 655;
8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sindbis virus. This sequence represents DNA used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 2; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX96938 standard; DNA; 655
                                                                                                                                                                         immunomodulatory cofactor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
WPI; 2003-174125/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX96938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX96938/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 27
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us-08-901-612a-58.rng

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within warm-blooded animals comprising administering to a warm-blooded animal a vector construct which directs the expression of at least one immunogenic portion of an antigen derived from an intracellular pathogen, and a protein having the immunogenic portion of the antigen to generate an immune response. The method is useful for treating intracellular infections or diseases including viral infections (e.g. hepatitis B virus (HBW), hepatitis C virus (HCW), herpes simplex virus (HSW), human immunodeficiency virus (HIV) or feline immunodeficiency virus (FIV)), parabitic infections (e.g. rickettsia, leishmaniasis or malaria) and certain bacterial diseases (e.g. leishmaniasis or malaria) and riss sequence represents hepatitis B virus DNA used in the method of the
          Human; HBV, HCV, gene; ds, hepatitis B virus; hepatitis C virus;
intracellular infection; HSV; HIV, viral infection; herpes simplex virus;
human immunodeficiency virus; FIV; feline immunodeficiency virus;
parasitic infection; rickettsia; malaria; leishmaniasis; tuberculosis;
                                                                                                                                                                                                                                                                                        Treating intracellular infections, e.g. viral, parasitic and bacterial diseases, comprises administering a vector construct which directs the expression of an immunogenic portion of an antigen from an intracellular
                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for treating intracellular infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 10; Length 655; 85.0%; Pred. No. 8.5; ative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 655 BP; 156 A; 171 C; 140 G; 188 T; 0 U; 0 Other;
                                                       bacterial disease; legionella; chlamydia
                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 44-45; 69pp; English.
                                                                                                                                                                                                                                             Lee WTL;
                                                                                                                                                  99US-00466035
                                                                                                                                                                        97US-00931031
                                                                                                                                                                                                                                           Sallberg M, Milich DR,
                                                                                                                                                                                                                                                                  WPI; 2003-288144/28
                                                                                                                                                                                             (SALL/) SALLBERG M. (MILI/) MILICH D R.
                                                                                                                                                                                                         (MILI/) MILICH D R
(LEEW/) LEE W T L.
                                                                             Hepatitis B virus
                                                                                                     US2002165172-A1.
                                                                                                                                                                        16-SEP-1997;
                                                                                                                                                  17-DEC-1999;
                                                                                                                            07-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                          pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

note = "Differs from the HB virus adw sequence published by Ono and associates (1983)"

*tag= g note= "As above"

.182

conflict

conflict

conflict

conflict

conflict

*tag= i note= "As above"

note= "As above"

*tag=

/*tag= k /note= "As above"

88WO-GB000663 87GB-00019108 88GB-00016084

11-AUG-1988; 12-AUG-1987; 12-JUL-1988;

23-FEB-1989. WO8901518-A.

(NATU-) NATURAL ENVIRON RES.

Bishop DH, Emery VC; WPI; 1989-068873/09.

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Gaps

. 0

AGAGAUGAUUAGGCAGAGGT 20 43 AGAGATGATTAGGCAGAGGT 24

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Local Similarity 85.0 nes 17; Conservative

Best Loca Matches

AAN91081/c ID AAN91081 standard; DNA; 660 BP.

RESULT 28

/*tag= j /note= "As above"

*tag= c 'note= "This is labelled 'preCore'"

Location/Qualifiers

Hepatitis B virus,

Φ

*tag= (*tag= (*t

misc_feature

33. .659 /*tag= d /note= "This labelled 'Core'" "Precore antigen"

/*tag= a /product= '

misc_feature

. .82

CDS

product= "Core Antigen"

.01. .658

CDS

*tag=

*tag= £

conflict

```
The coding sequences of the preC and C Ags of HB virus were inserted into Autograph californica muclear polyhedrosis virus (ACNPV) transfer vector packMixTyc and packMixTyc recombinant transfer vectors were called packMixTyc and packMixTyc. Following cotransfection with infectious AcNPV DNA, recombinant baculoviruses were obtained - YMIXYc and YMIXYc. It was determined that all the HBcAg and HBpcAg was cell associated and that the yield of purified HBcAg was of the order of 5 mg per liter of 1x10(9) infected cells. Such Ag may be useful in vaccines. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                   New plasmid replicon for inserting several genes into vector - contg. two polypeptide expression structures, and derived viral vectors for infecting insect cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 660 BP; 156 A; 171 C; 143 G; 189 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                   Disclosure, Page ?; 74pp; English.
P-PSDB; AAP90702
```

100.0%; Score 20; DB 1; Length 660; 85.0%; Pred. No. 8.5;

Query Match Best Local Similarity

of subclones encompassing the core (C) and precore (preC) of an adw serotype hepatitis B (HB) virus.

(first entry)

DNA sequence of antigens (Ag)

(revised)

25-MAR-2003 14-JUL-1990

AAN91081;

Hepatitis B virus; core gene; precore gene; antigen; vaccine; polypeptide expression sequence; ACNPV transfer vector pAcYMI; pAcYMIKTpc; pAcYMIKTpc; recombinant baculovirus; YMIKYpc; MXIKTpc.

Page 16

RESULT 30

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Gaps

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Indels

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3; Mismatches

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Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                           Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBSAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBeAg; ds.
                                                                                                                          HBV genotype G strain US6 preCore/Core DNA.
                 1 AGAGAUGAUUAGGCAGAGGT 20
                         46 AGAGATGATTAGGCAGAGGT 27
                                                                  572/c
AAH77572 standard; DNA; 664 BP
                                                                                                                                                                                                                             20-NOV-2000; 2000WO-EP011526.
                                                                                                                                                                                                                                               99EP-00870252
99US-0169287P
                                                                                                           (first entry)
17; Conservative
                                                                                                                                                                                                                                                                                        Van Geyt C,
                                                                                                                                                                                                                                                                       (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                         WPI; 2001-374785/39.
                                                                                                                                                                             Hepatitis B virus.
                                                                                                                                                                                             WO200140279-A2.
                                                                                                                                                                                                                                              03-DEC-1999;
07-DEC-1999;
                                                                                                           19-OCT-2001
                                                                                                                                                                                                              17-JUN-2001
                                                                                                                                                                                                                                                                                         Stuyver L,
                                                                                          AAH77572;
                                                                                                                                                                                                                                                                                                                                                  therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an HBV
Matches
                                                         RESULT 29
AAH77572/C
                                                                         셤
                 ò
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De Gendt S;

human hepatitis B virus the complete independence of a new human hepatitis B virus that a high prevalence in patients of an eventual genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention relates to a fully defined sequence of 3248 mucleotides as given in specification, a sequence with 92% identity to the given sequence, or specification, a sequence with 92% identity to the given sequence, or polynucleotides are useful for mentioned sequences. These polynucleotides are useful for detecting antibodies in a biological the proteins are useful for detecting antibodies in a biological the proteins are useful for detecting the proteins and for detecting the proteins and sor detecting the proteins and sor detecting the proteins and antibodies directed against the proteins are useful for detecting the proteins and sor detecting the proteins and antibodies of a detecting the proteins and an elso useful for preparing a vaccine or medicament for treating HBV infections. The t sequence is provided in an alignment of preCore/Core sequences of genotype A strain (HBVXCPS) and 7 strains (FR1, FR2, US1, US3, The invention relates to the complete nucleic acid sequence of Claim 3; Fig 7; 94pp; English.

US6, US7, US9, US10) of HBV genotype G present sequence is

Sequence 664 BP; 146 A; 160 C; 144 G; 208 T; 0 U; 6 Other;

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Gaps
                            .
 ; Score 20; DB 4; Length 664; Pred. No. 8.5; 3; Mismatches 0; Indels
                           0; Indels
100.08;
              85.0%;
                        17; Conservative
           Local Similarity
Query Match
                        Matches
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Gaps

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Query Match 100.0%; Score 20; DB 12; Length 669; Best Local Similarity 85.0%; Pred. No. 8.5; Matches 17; Conservative 3; Mismatches 0; Indels C

20 44

63 AGAGATGATTAGGCAGAGGT

1 AGAGAUGAUUAGGCAGAGGT

8 셤

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1 AGAGAUGAUUAGGCAGAGGT 20
       33
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Modulating a systemic immune response to a peptide in a mammal comprises transmucosally administering a macromolecular aggregate of the peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                   a HBV protein. A monomolecular peptide is useful for the induction of oral tolerance when induction of systemic immunity is undesirable, e.g. in cases of chronic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 669 BP; 155 A; 170 C; 148 G; 196 T; 0 U; 0 Other;
                                                                  HBcAg; immunomodulator; vaccine; gene; ss.
                                                                                                                                   'note= "No start codon"
                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 1; 81pp; English.
                                                                                                Location/Qualifiers
                                                    Hepatitis B virus core antigen DNA
                                                                                                              *tag= a
product= "HBcAg"
ADO07220/c
ID AD007220 standard; DNA; 669 BP.
                                                                                                                                                                               17-OCT-2003; 2003WO-US033178.
                                                                                                                                                                                             17-OCT-2002; 2002US-0419279P.
                                                                                                                            partial
                                                                                                                                                                                                                                        WPI; 2004-348329/32.
P-PSDB; AD007221.
                                                                                                                                                                                                           (ORAG-) ORAGEN CORP.
                                                                                 Hepatitis B virus.
                                                                                                                                                 WO2004035007-A2.
                                     15-JUL-2004
                                                                                                                                                                 29-APR-2004.
                                                                                                                                                                                                                         Michaels F;
                       ADO07220;
                                                                                               Key
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1.8

The present sequence

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The present invention relates to hepatitis B virus (HBV) strain FRI, press and surface antigen HBAG) and HBX protein, HBpOl, envelope (Presi, Press and surface antigen HBAG) and HBX proteins. HBV genotype G nucleic acids and polypeptides are useful for diagnosing, prognosing and treating infections caused by HBV genotype G. They can be used in a vaccine to treat or prevent HBV genotype G. They can be used in a vaccine to nucleic acids and antibodies are useful for detecting HBV genotype G derived nucleic acids and antibodies are useful for detecting HBV genotype G in sample or diagnosis of HBV genotype G infection. The presence of HBV genotype G statistically correlates with the presence of HBV peptide encoding nucleic acid is useful for designing monitoring assays and HBAG (genotype G entiged) in patients infected with HBV. The antibodies or antigens of HBV genotype G are useful for identifying a
                                                                                                                                                                                                                                                                                                                       \[\text{transl_except= (pos:4. .6, aa.Xaa)}\]
\[\text{transl_except= (pos:82. .84, aa.Xaa)}\]
\[\text{note= "Xaa corresponds to in-frame stop codon; Does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel hepatitis B virus genotype G, nucleic acids encoding virus, polypeptides encoded by nucleic acids, useful for preparing vaccine to treat or prevent the hepatitis B virus genotype G infection in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ̈́
                                                                                                                                                          HBV genotype G; precore; HBpol; polymerase; envelope protein; preSl; preS2; surface antigen; HBsAg; HBX protein; vaccine; liver disease; hepatitis; liver cancer; HBCAg; core antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fried
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zoulim F,
                                                                                                                            Hepatitis B virus FR1 strain genotype G PreCore/HBcAg DNA
                                                                                                                                                                                                                                                                                                        product= "PreCore/HBcAg core protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De Gendt S, Van Geyt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= d
/note= "Core insert peptide DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/note= "HBcAg core protein DNA"
                                                                                                                                                                                                                                                                                                                                                                                                      . .87
*tag= b
note= "PreCore protein DNA"
                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 56-57; 84pp; English
                               AAD09092 standard; DNA; 673 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-2000; 2000WO-US032108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0167206P
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94. .129
                                                                                                                                                                                                                                                                                                                                                                                          partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                     38. .672
                                                                                                                                                                                                                                                                          .672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PHAR-) PHARMASSET INC. (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schinazi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-367676/38.
P-PSDB; AAE04707.
                                                                                                                                                                                                                           Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200138498-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                            04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stuyver L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rossau R;
                                                              AAD09092;
RESULT 31
AAD09092/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Burope and the USA. The invention relates to a fully defined sequence of 1348 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These the polynucleotides are useful for the yenotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and antibodies directed against the proteins are useful for detecting the proteins and for detecting the proteins and succeeding a vaccine or medicament for treating HBV infections. The present sequence is the complete coding sequence of the HBV preCore/Core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBV); HBPOl; HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBcAg; ds.
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                                                                                                                                           Gaps
stage of liver disease caused by HBV genotype G. The present sequence hepatitis B virus (HBV) strain FR1, genotype G DNA fragment encoding PreCore/Core antigen (HBCAg) protein
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                                                                                                       DB 4; Length 673;
8.5;
                                                                       Sequence 673 BP; 148 A; 165 C; 146 G; 214 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 675 BP; 149 A; 165 C; 147 G; 214 T; 0 U; 0 Other;
                                                                                                                       85.0%; Pred. No. 8.5.
                                                                                                        100.0%; Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De Gendt S;
                                                                                                                                                                            1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                 33 AGAGATGATTAGGCAGAGGT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 2; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2000; 2000WO-EP011526.
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99US-0169287P
                                                                                                                                                                                                                                                                                                      AAH77563 Btandard; DNA; 675
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                                                                                                                         Local Similarity 85.0
ses 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stuyver L, Van Geyt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                             HBV preCore/Core gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-374785/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
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07-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                       AAH77563;
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                                                                                                          Query Match
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Matches
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AAH77567/c ID AAH77567 standard; DNA; 681 BP.

AAH77567;

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Hepatitis B virus, HBV, preCore, Core, preSl, preS2, HBS, HBX, HBPOl, HB8Ag; antiviral, vaccine, genotype G; genotype A; genotyping, HBcAg;
                                                                                                                                                                                                                                                                                                                              Novel isolated and/or purified hepatitis B virus polypeptide and bolynuclectide sequences that are phylogenetically different from genotype A-F molecules, useful for HBV diagnosis, prophylaxis and therapy.
                                                                                                                 HBV genotype A strain HBVXCPS preCore/Core DNA.
                                                                                                                                                                                                                                                                                             De Gendt S;
20
          33 AGAGATGATTAGGCAGAGGT 14
                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 7; 94pp; English.
                                                             AAH77566 standard; DNA; 681 BP
1 AGAGAUGAUUAGGCAGAGGT
                                                                                                                                                                                                                             20-NOV-2000; 2000WO-EP011526.
                                                                                                                                                                                                                                                         99US-0169287P
                                                                                                                                                                                                                                              03-DEC-1999; 99EP-00870252
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                         (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                           Stuyver L, Van Geyt C,
                                                                                                                                                                                                                                                                                                             WPI; 2001-374785/39.
                                                                                                                                                                         Hepatitis B virus.
                                                                                                                                                                                         WO200140279-A2.
                                                                                                 19-OCT-2001
                                                                                                                                                                                                                                                        07-DEC-1999;
                                                                                                                                                                                                           07-JUN-2001
                                                                                                                                                       HBeAg; ds.
                                                                              AAH77566;
8
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The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients Chronically infected with HBV and residing in Europe and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92% identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polynucleotides are useful for HBV genotyping. The proteins encoded by the polynucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and for detecting the proteins and for detecting the proteins and for detecting the proteins are useful for detecting the proteins and for detecting many and the proteins are useful for preparing a vaccine or medicament for treating HBV infections. The present sequence is provided in an alignment of precore/Core sequences of an HBV genotype A strain (HBVXCPS) and 7 strains (FRI, FRZ, USI, USS, USI), USS, USI, USS, USI) of HBV genotype G

ö Gaps ; 0 ; Score 20; DB 4; Length 681; Pred, No. 8.5; 0; Indels 3; Mismatches 0; Indels Sequence 681 BP; 151 A; 166 C; 139 G; 189 T; 0 U; 36 Other; 100.0%; l Similarity 85.0%; 17; Conservative Local Similarity Query Match Matches

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RESULT 34

BP.

AAN80943 standard; DNA; 750

RESULT 35

(revised)
(first entry)

25-MAR-2003 19-NOV-1990

AAN80943;

AAN80943/c
ID AAN8094
XX
AC AAN8094
XX
DT 25-MARDT 19-NOV-

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                                                            Hepatitis B virus; HBV; preCore; Core; preSl; preS2; HBS; HBX; HBPOl;
HBsAg; antiviral; vaccine; genotype G; genotype A; genotyping; HBcAg;
HBeAg; ds.
                                                                                                                                                                                                                                                 Novel isolated and/or purified hepatitis B virus polypeptide and polynucleotide sequences that are phylogenetically different from HBV genotype A-F molecules, useful for HBV diagnosis, prophylaxis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 4; Length 681;
8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 681 BP; 149 A; 165 C; 147 G; 214 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                  HBV genotype G strain FR1 preCore/Core DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB
85.0%; Pred. No. 8.5;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             US6, US7, US9, US10) of HBV genotype G
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                                                                                                                                                                                                                   De Gendt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                             Claim 3; Fig 7; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAGATGATTAGGCAGAGGT
                                                                                                                                                      20-NOV-2000; 2000WO-EP011526.
                                                                                                                                                                                 99US-0169287P
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 85.0
les 17; Conservative
                                                                                                                                                                                                                  Van Geyt C,
                                                                                                                                                                                                (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                  WPI; 2001-374785/39.
                                                                                                    Hepatitis B virus.
                                                                                                                     WO200140279-A2.
                                                                                                                                                                       03-DEC-1999;
07-DEC-1999;
                                 19-OCT-2001
                                                                                                                                     07-JUN-2001
                                                                                                                                                                                                                  Stuyver L,
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                                                                                                                                                                                                                                                                                                                                                                                                        The cloned HBV DNA can be used to engineer plasmids for HBCAg synthesis in bacteria. The DNA may be fused to a gene for beta galactosidase. The recombinant protein can be used for immuno- assays, to raise antibodies, and in vaccines. See also AAN82265 and 66. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic mouse; cancer; oncogene; bicistronic hepatitis B virus; HBV; X15-c-myc transgene; hepatocellular carcinoma; malignant liver tumour; X15; c-myc; murine; HBX; carcinogen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                          Polynucleotide encoding HBEAG and HBCAG immuno-reactive polypeptide useful in immunoassays, for raising antibodies and as vaccine prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 100.0%; Score 20; DB 1; Length 750; Local Similarity 85.0%; Pred. No. 8.6; nes 17; Conservative 3; Mismatches 0; Indels
                                     Hepatitis B core antigen; virus; vaccine; immunoassay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 750 BP; 176 A; 192 C; 160 G; 222 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                              Staller JM;
                                                                                                                                                                                                                                                                              Mimms LT,
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page ?; 32pp; English.
                                                                                                  31. .675
/*tag= a
/product= "HBcAg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGAGAUGAUUAGGCAGAGGT 20
           HBV core gene of plasmid pHBV-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH77169 standard; DNA; 909 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAGATGATTAGGCAGAGGT
                                                                                                                                                                                                     87EP-00117370
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                                                                                                                                                                                                                            86US-00944645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                       WPI; 1988-176639/26
                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAB
                                                            Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B virus
                                                                                                                                                                                                                                                                                                                    P-PSDB; AAP80961
                                                                                                                                                                                                                                                                               Andersen PR,
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                                                                                                                                                                            29-JUN-1988
                                                                                                                                                   EP272483-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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this purputation to the regions of the registatory and cooling regions of the XIS component in the X-myc construct. The invention comprising of the XIS component in the X-myc construct. The invention comprising of the HBV XIS gene and c-myc gene. The myc gene is known to comprising of the HBV XIS gene and c-myc gene. The myc gene is known to brotein that has amino acids S8-154 of HBV XIS and a murine c-myc protein, respectively. A transgenic mouse contending the transgene construct is useful for screening acandidate substance (CS), to determine whether CS promotes hepatocellular carcinoma. This is construct be exposed a candidate substance (CS), to determine by exposing a transgenic mouse to CS, and monitoring the mouse core for the development of hepatocellular carcinoma, where an increase in the development of hepatocellular carcinoma, where an increase in the transgenic mouse not exposed to CS, indicates that CS promotes a compared to the development of hepatocellular carcinoma in a transgenic mouse not exposed to CS, indicates that CS promotes CC for call and tissue culture. The transgenic mine employed as a source constrained by transgenic mine for hepatocellular carcinoma are superior to the HBV XIS-c-myc transgene for hepatocellular carcinoma are superior to any transgenic minel models bystem for hepatocellular carcinoma in that carcinoma tiver tumours in all lobes causing death of the affected mainals in 20-22 weeks, that is faster than the time taken by the other caransgenic animals to even develop a tumour
                                                                                                                                                                                                                                                          This polynuclectide represents the sequence of the regulatory and coding
                                                                                                                                   New bicistronic hepatitis B virus (HBV) X15-c-myc transgene, useful for producing transgenic mouse model systems for human hepatocellular carcinoma, comprises HBV X15 transgene and c-myc transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 909 BP; 210 A; 236 C; 211 G; 252 T; 0 U; 0 Other;
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(ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
(NAIM-) NAT INST IMMUNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20;
                                                           Anand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGAGAUGAUUAGGCAGAGGT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
85.0%; P
                                                                                                                                                                                                                   Claim 3; Fig 3; 12pp; English.
                                                           Totey S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HBV-related disease; ss.
                                                                                                WPI; 2002-009266/01
                                                           Singh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus.
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                                                           Kumar V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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AAV82691/c
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98WO-EP002048. 97GB-00007221.

UNIU) UNIV GLASGOW

Carman B;

39-APR-1997; 08-APR-1998;

Thu Dec 16 14:59:49 2004

WPI; 1999-009329/01. WPI; 1999-009329/01. WO9845421-A2. 08-APR-1998; 09-APR-1997; 15-OCT-1998. Fulminant Query Match AAV82688; Carman B: ò g

The present sequence represents part of the genome of a fulminant the specification describes Hepatitis B virus (HBN) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBN) nucleotide and that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II, core upstream regulatory sequence, basal core promoter region, or a mutation which leads to an X-peptide anno acid change to Cys or Met. The HBV variants of the proteins and HBV nucleic acid. Probes that hybridise to any of the proteins and the region are used to detect binding interactions between host or viral specified mutated regions are used to detect HBV-related disease. New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic. especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell Gaps ö 100.0%; Score 20; DB 2; Length 1334; 85.0%; Pred. No. 9.2; Sequence 1334 BP; 288 A; 363 C; 311 G; 372 T; 0 U; 0 Other; 0; Indels 3; Mismatches Disclosure; Fig 5; 85pp; English. 1 AGAGAUGAUUAGGCAGAGGT 20 Best Local Similarity 85.0%; Matches 17; Conservative

AAV82688 standard; DNA; 1395 BP

(first entry) 16-FEB-1999 Fulminant hepatitis B virus genotype D variant FHBV5 sequence.

hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; ss.

Hepatitis B virus.

98WO-EP002048.

97GB-00007221.

(UNIU) UNIV GLASGOW

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure, Fig 5, 85pp, English.

The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.

The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, or a mutation which leads to a sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell

88333333333333333

Sequence 1395 BP; 277 A; 387 C; 331 G; 398 T; 0 U; 2 Other;

Gaps ö 100.0%; Score 20; DB 2; Length 1395; 85.0%; Pred. No. 9.2; ive 3; Mismatches 0; Indels 1 AGAGAUGAUUAGGCAGAGGT 20 17; Conservative Best Local Similarity Matches 17; Conserv Query Match ઠે

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뗦. AAV82687 standard; DNA; 1400 AAV82687; AAV82687/

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Fulminant hepatitis B virus genotype D variant FHBV4 sequence. (first entry) 16-FEB-1999

B virus; variant; FHBV; HBV; binding interaction; Fulminant hepatitis B vi HBV-related disease; ss.

Hepatitis B virus.

WO9845421-A2.

15-0CT-1998

98WO-EP002048. 08-APR-1998; 97GB-00007221. 09-APR-1997;

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure, Fig 5, 85pp, English.

The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory peptide amino acid change to Gy so Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, specified mutated regions are used to detect HBV-related disease, especially fullminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; 88.

Hepatitis B virus. WO9845421-A2. 98WO-EP002048. 97GB-00007221.

08-APR-1998; 09-APR-1997;

15-0CT-1998

UNIU) UNIV GLASGOW

Carman B;

Fulminant hepatitis B virus genotype D variant FHBV2 sequence.

16-FEB-1999

AAV82685;

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846 AGAGATGATTAGGCAGAGGT 827

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AAV82685 standard; DNA; 1445 BP

AAV82685,

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The present sequence represents part of the genome of a fulminant thepatitis B virus (FRBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral
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mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pulminant hepatitis B virus genotype D variant FHBV13 sequence.
                                                                                                                                                                              100.0%; Score 20; DB 2; Length 1400; 85.0%; Pred. No. 9.2; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1445 BP; 297 A; 406 C; 338 G; 404 T; 0 U; 0 Other;
                                                                                                           Sequence 1400 BP; 287 A; 388 C; 332 G; 393 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                     846 AGAGATGATTAGGCAGAGGT 827
                                                                                                                                                                                                                                                                                                                                             1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 5; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV82692 standard; DNA; 1445 BP.
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                                                                                                                                                  16-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HBV-related disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNIU ) UNIV GLASGOW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV82692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carman B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV82692/
XX AAV82692/
XXX AAV8
XXX AAV8
XXX AAV8
XXX Hepa
XXX Hep
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The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nuclectides 1000 to 2500.

The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, to a mutation which leads to an x-peptide amino acid change to Cys or Met. The HBV variants of the reported amino acid change to Cys or Met. The HBV variants of the proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especified mutated forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                               New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 2;
85.0%; Pred. No. 9.2;
ive 3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 5; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV82690 standard; DNA; 1445 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-009329/01.
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ID AAV82
XX
AC AAV82
XX
DT 16-FI
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16-FEB-1999 (first entry)

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Gaps

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0; Indels

100.0%; Score 20; DB 2; Length 1445;

Best Local Similarity 85.0%; Pred. No. 9.2; Matches 17; Conservative 3; Mismatches

Query Match

1 AGAGAUGAUUAGGCAGAGGT 20

us-08-901-612a-58.rng

97GB-00007221. 98WO-EP002048

08-APR-1998; 09-APR-1997; (UNIU) UNIV GLASGOW

WPI; 1999-009329/01.

Carman B;

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The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the proteins and environment of the contractions are used regions are used to detect HBV-related disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   because they
                                        Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
HBV-related disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because treduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                                                                                                                                                                                                                                                                                                             New hepatitis B virus nucleic acid with combination of specific mv - useful for, e.g. detection of binding interactions between host viral proteins and HBV nucleic.
Fulminant hepatitis B virus genotype D variant FHBV7 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1445 BP; 293 A; 402 C; 340 G; 410 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 5, 85pp, English.
                                                                                                                                                                                                                               98WO-EP002048
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                                                                                                                                                                                                                                                                                                         (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-009329/01.
                                                                                                       Hepatitis B virus
                                                                                                                                              WO9845421-A2
                                                                                                                                                                                                                           08-APR-1998;
                                                                                                                                                                                                                                                                    09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (FHBV) undicic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative crequiatory element region, the enhancer I/ core upstream regulatory squence/ basal core promoter region, or a mutation which leads to an X-sequence/ basal core promoter to Met. The HBV variants of the peptide amino acid change to Cys or Met. The HBV variants of the proteins and HBV nucleic acid. Probes that hybridise to any of the proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to detect HBV-related disease.

Specified mutated regions are used to detect HBV-related clisease.

Specified mutated regions are used to detect Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure; Fig 5; 85pp; English.

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                                                                                                                                                                                                                                                                                                                                                                   Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
HBV-related disease; ss.
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                      Fulminant hepatitis B virus genotype D variant CHBV2 sequence.
                                                                                                                                                                                                                                      Length 1445;
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                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                     , DB 2;
9.2;
                                                                                                                                                                                                                                           85.0%; Pred. No. 9.2; ive 3; Mismatches
                                                                                                                                                                                                                                    100.0%; Score 20;
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                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                               1 AGAGAUGAUUAGGCAGAGGT
                                                                                                                                                                                                                                                                                               RESULT 44
AAV82695/c
ID AAV82695 standard; DNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-EP002048.
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIU ) UNIV GLASGOW
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Gaps

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846 AGAGATGATTAGGCAGAGGT 827

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AAV82684 standard; DNA; 1445

1 AGAGAUGAUUAGGCAGAGGT 20

Best Local Similarity 85.0 Matches 17; Conservative

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; ss.

Hepatitis B virus.

WO9845421-A2 15-0CT-1998

Fulminant hepatitis B virus genotype D variant FHBV1 sequence.

(first entry)

16-FEB-1999

AAV82684;

ò - useful for, e.g. detection of binding interactions between host viral proteins and HBV nucleic.

Disclosure; Fig 5; 85pp; English

The specification describes Hepatitis B virus (HBV) nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell sequence represents part of the genome of a

Sequence 1500 BP; 308 A; 412 C; 347 G; 433 T; 0 U; 0 Other;

Gapa ö Score 20; DB 2; Length 1500; Pred. No. 9.3; 0; Indels Mismatches 3; 100.0%; 85.0%; E Conservative Local Similarity 17; Query Match Matches

1 AGAGAUGAUUAGGCAGAGGT 20

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RESULT 45 AAV82683/

683/c AAV82683 standard; DNA; 1500

BP

AAV82683;

(first entry) 16-FEB-1999 Fulminant hepatitis B virus genotype D variant AHBV1 sequence.

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;

HBV-related disease; ss.

Hepatitis B virus.

WO9845421-A2

15-OCT-1998

98WO-EP002048. 08-APR-1998; 97GB-00007221. 09-APR-1997;

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure; Fig 5; 85pp; English

The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory

especially fullment infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell or a mutation which leads to an Xpeptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease. promoter region, sequence/ basal core 8\$33333333333

Seguence 1500 BP; 305 A; 411 C; 354 G; 430 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 20; DB 2; Length 1500; 85.0%; Pred. No. 9.3; ive 3; Mismatches 0; Indels Query Match 100. Best Local Similarity 85.0 Matches 17; Conservative

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20 1 AGAGAUGAUUAGGCAGAGGT

8 ద RESULT 46

BP. AAV82694/c ID AAV82694 standard; DNA; 1500

AAV82694;

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16-FEB-1999 (first entry

Fulminant hepatitis B virus genotype D variant HBVP2CSX sequence.

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; ss.

Hepatitis B virus.

WO9845421-A2.

98WO-EP002048 08-APR-1998;

97GB-00007221 09-APR-1997;

GLASGOW VINU (UINU)

Carman B;

WPI; 1999-009329/01.

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure, Fig 5, 85pp, English.

Hepatitis B virus (FHBV) genotype D variant, mucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell present sequence represents part of the genome of a fulminant

Sequence 1500 BP; 305 A; 408 C; 349 G; 438 T; 0 U; 0 Other;

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; ss.

Hepatitis B virus. WO9845421-A2

Fulminant

98WO-EP002048. 97GB-00007221.

08-APR-1998; 09-APR-1997;

L5-OCT-1998.

UNIU) UNIV GLASGOW

WPI; 1999-009329/01.

Carman B;

Wild type hepatitis B virus genotype D nucleotides 1000-2500.

(first entry)

16-FEB-1999

AAV82706;

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Gaps

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AAV82706 standard; DNA; 1500 BP.

AAV82706/c

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The present sequence represents part of the genome of a fulminant Hepatitis B virus (FHBV) genotype D variant, nucleotides 1000 to 2500.

The specification describes Hepatitis B virus (FHBV) uncleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, or a mutation which leads to an X-sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease. Competing ally fulminant infection, but also severe chronic infection or serologically fulminant infection, but also severe chronic infection or serologically numenal forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fulminant hepatitis B virus, variant, FHBV, HBV, binding interaction, HBV-related disease, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fulminant hepatitis B virus genotype D variant FHBV3 sequence.
    ch 100.0%; Score 20; DB 2; Length 1500; Similarity 85.0%; Pred. No. 9.3; 17; Conservative 3; Mismatches 0; Indels (
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                                                                                                                                                                                                      1 AGAGAUGAUUAGGCAGAGGT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAV82686 standard; DNA; 1500 BP
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                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV82686;
                                                                                                                                                                                                                                                                                                                                   RESULT 47
AAV82686/C
AAV82686/C
XX
AAV82686/C
XX
DT 16-FEB
XX
DE Fulmin
XX
KW Fulmin
XX
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New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Disclosure; Fig 5; 85pp; English.

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The present sequence represents part of the genome of wild type Hepatitis B virus genotype D, nucleotides 1000 to 2500. Mutations occur in this region in fulminant hepatitis B virus (FHBV) patients. The specification describes Hepatitis B virus (FHBV) patients. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in the last two of the enhancer I region, the negative requlatory element region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or scrologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fulminant hepatitis B virus genotype D variant FHBV6 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 2; Length 1500; 85.0%; Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1500 BP; 304 A; 409 C; 351 G; 436 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGAGAUGAUUAGGCAGAGGT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV82689 standard; DNA; 1500 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV82689;
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1D AAV8266
XX AC AAV8266
XX I6-FEB.
XX DE Fulmin.
KW Fulmin.
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Gaps

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'Match 100.0%; Score 20; DB 2; Length 1500; Local Similarity 85.0%; Pred. No. 9.3; es 17; Conservative 3; Mismatches 0; Indels (

Query Match

Best Loca Matches

RESULT 48

1 AGAGAUGAUUAGGCAGAGGT 20

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Hepatitis B virus (FREW) genoty pour out the general conditions of a virus (FREW) genoty pour out the specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (i.e. alteration from the normal nucleotide in any of the genotypes A to F) in at least two of the enhancer I region, the negative regulatory element region, the enhancer II/ core upstream regulatory peptide amino acid change to Gy sor Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or serologically nunsual forms of disease. Combinations of the specified
                                                                                                                                                                                                                                                                                                                                         New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probably because they
                                                                                                                                                                                                                                                                                                                                                                                                                                                          represents part of the genome of a fulminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutations are associated with fulminant infections, probably be reduce the ability to bind inhibitory proteins in the host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1500 BP; 302 A; 416 C; 353 G; 427 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 5, 85pp; English
                                                                                                                                                  98WO-EP002048
                                                                                                                                                                                        97GB-00007221
HBV-related disease;
                                                                                                                                                                                                                          (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                                                                     WPI; 1999-009329/01.
                                     Hepatitis B virus.
                                                                         WO9845421-A2
                                                                                                                                                  08-APR-1998;
                                                                                                                                                                                        09-APR-1997;
                                                                                                             15-OCT-1998
                                                                                                                                                                                                                                                                   Carman B;
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Gaps ö 100.0%; Score 20; DB 2; Length 1500; 85.0%; Pred. No. 9.3; 0; Indels Pred. No. 9.3; 3; Mismatches 17; Conservative Local Similarity Query Match Best Loca Matches

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AAV82693 standard; DNA; 1500 AAV82693;

Fulminant hepatitis B virus genotype D variant HBVP3CSX sequence. 16-FEB-1999 (first entry)

Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction;

HBV-related disease; ss.

Hepatitis B virus

WO9845421-A2

15-OCT-1998

98WO-EP002048 08-APR-1998;

97GB-00007221 09-APR-1997;

(UNIU) UNIV GLASGOW

Carman B;

WPI; 1999-009329/01

New hepatitis B virus nucleic acid with combination of specific mutations - useful for, e.g. detection of binding interactions between host or viral proteins and HBV nucleic.

Hepatitis B virus (FREV) genotype D variant, mucleotides 1000 to 2500. The specification describes Hepatitis B virus (HBV) nucleic acid that has a mutation (1.e. alteration from the normal nucleotide in any of the genotypes A to P) in at least two of the enhancer I region, the negative region, the enhancer II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. The HBV variants of the invention are used to detect binding interactions between host or viral proteins and HBV nucleic acid. Probes that hybridise to any of the specified mutated regions are used to detect HBV-related disease, especially fulminant infection, but also severe chronic infection or serologically unusual forms of disease. Combinations of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell sequence represents part of the genome of a fulminant Disclosure; Fig 5; 85pp; English.

Sequence 1500 BP; 314 A; 403 C; 343 G; 440 T; 0 U; 0 Other;

Gaps ö Length 1500; 0; Indels ; Score 20; DB 2; Pred. No. 9.3; 3; Mismatches 0; 85.0%; 17; Conservative Query Match Best Local Similarity Matches

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